

Db 327 DMIPALPSFSTLE-NLLRKPDPFTLLQEIIRMYTSFRQNGTIEYNNYWGQRLTSLYIYG 385  
QY 386 NGIFORMGTTNDLRNIDFQADVYKI-----TSLAINMLVGETTAR 428  
Db 386 SS-FNKYSGLVGAEDIIIPVGQNDIYRVVMTVIGRYTNLLGWNVPVTFYFSNNTQKTSYK 444  
QY 429 PEY---RVSKADFRVGGPDL---NYDAGNGLSRMT---IESTPLVLHSGVGRGPSHR 479  
Db 445 PKQFAGGKITD---SGBELTYENQSYSHRVSYITSPEIKSTGGTVL---GV----- 491  
QY 480 LSNAACVVYGNRVNRYGTHTSKRENIIEANQITQIPAVKSYLYQLQNYLANAYTYVIKG 539  
Db 492 -----VPIFGWTHSSASRNNFIYATKISQIPINKA---SRTSGGAVNMFQEG 535  
QY 540 THTGDLIRFLRTKSEYNAVYAGG-----IRLIINNKTAGQSYRIRFRYAADKAPFSV 594  
Db 536 LYPGGMGNRFRVSLKSYSGNY-----DLKYSDPKFAEIIITPPLSSNIQMDVE 645  
QY 595 YLYPGGMGNRFRVSLKSYSGNY-----DLKYSDPKFAEIIITPPLSSNIQMDVE 645  
Db 585 -----SSRSPENPATYSASIAYTNTMTNASTYSTFAYAE-----SGPINLGIS 629  
QY 646 MOANSFQSDV-----NVLDKIEFLPSNTTTLBYEGERDLEKTKNAVNDLFTN 693  
Db 630 GSSRTFDISITKEAGANLYIDRIEIPVNTL---FEAEDLDVAKKAVNGLFTN 681

## RESULT 10

US-08-272-887-2  
; Sequence 2, Application US/08272887  
; Patent No. 5747450  
; GENERAL INFORMATION:  
; APPLICANT: Ohba, Michio  
; APPLICANT: Iwahana, Hidenori  
; APPLICANT: Sato, Reichi  
; APPLICANT: Suzuki, No. 5747450ukazu  
; APPLICANT: Ogiwara, Katsutoshi  
; APPLICANT: Sakanaka, Kazunobu  
; APPLICANT: Hori, Hidetaki  
; APPLICANT: Asano, Shouji  
; APPLICANT: Kawasugi, Tadaaki  
; TITLE OF INVENTION: No. 5747450el Microorganism and Insecticide  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: US  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/272,887  
; FILING DATE: 08-JUL-1994  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/915,203  
; FILING DATE: 23-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: M/K 301  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1149 amino acids

; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-272-887-2  
Query Match 19.9%; Score 728.5; DB 1; Length 1149;  
Best Local Similarity 29.9%; Pred No. 3.2e-55;  
Matches 232; Conservative 124; Mismatches 240; Indels 179; Gaps 34;  
QY 4 MSPYONKNEYEILESSNNTNTPN---RYPPANNRDMSTMWDCQGISWDE----- 52  
Db 1 MSP-NNQNEYEIIIDALSPTSVSDNSIRYPLANDQTNLQNNMYKDYLKWTESTNAELSRN 59  
QY 53 --IWESVETIISIGINLIEFVIE-----PSLGINVTL--SIIGKLIPTRQTVSALSICDL 105  
Db 60 PGTFSIAQDAVGTGIDIVSTIIISGLGIPVLGEVFSILGLLWPSNNENVMQIFMVRV 119  
QY 106 LSIRKEVADSVLSADADFGKLNVR---EYVLSYLGAWLKDGKPLQKTNNSDIGQLV 162  
Db 120 BELIDQKILDSVRBRATAD---LANSRIAYEYQNALEDNRKRP---HSTRSAAL----- 168  
QY 163 YFFKLSEDFN--BILG---GSLSRNNAQVLLLPFFAQAANVQLLLLRDVAVOYKAQWPPF 217  
Db 169 ---VKERFGNAEAILRTNMGSPSQTNVETPLPTYAQAASLHLVMDVDVQIYKEMG-- 222  
QY 218 LSAENVRELISPNSGCDFTGDYERLCKTAETNYCLYVYQVGLNQIKOGGTGADTWS 277  
Db 223 -----YPQNDIDL---FYKEQVSYTARYSDHCQVQYNAGLNKLR---GTGAKQMV 266  
QY 278 KFNKPRREMTLAVLDIIAIPPTYDPEKYPLPHTHVELTREIYTDVAG--YSSGTYSWLRNWP 336  
Db 267 DYNFRFRREMMVMDLVALFNYDARIYPLETNAELTREIFTDPVGSVTVQSSLTLSWY 326  
QY 337 N-----TFNGLEANGTRGPGELVTWLSKIGIYNEY---VSRYPAGVWGTTHYEDYTKG 385  
Db 327 DMIPALPSFSTLE-NLLRKPDPFTLLQEIIRMYTSFRQNGTIEYNNYWGQRLTSLYIYG 385  
QY 386 NGIFORMGTTNDLRNIDFQADVYKI-----TSLAINMLVGETTAR 428  
Db 386 SS-FNKYSGLVGAEDIIIPVGQNDIYRVVMTVIGRYTNLLGWNVPVTFYFSNNTQKTSYK 444  
QY 429 PEY---RVSKADFRVGGPDL---NYDAGNGLSRMT---IESTPLVLHSGVGRGPSHR 479  
Db 445 PKQFAGGKITD---SGBELTYENQSYSHRVSYITSPEIKSTGGTVL---GV----- 491  
QY 480 LSNAACVVYGNRVNRYGTHTSKRENIIEANQITQIPAVKSYLYQLQNYLANAYTYVIKG 539  
Db 492 -----VPIFGWTHSSASRNNFIYATKISQIPINKA---SRTSGGAVNMFQEG 535  
QY 540 THTGDLIRFLRTKSEYNAVYAGG-----IRLIINNKTAGQSYRIRFRYAADKAPFSV 594  
Db 536 LYPGGMGNRFRVSLKSYSGNY-----DLKYSDPKFAEIIITPPLSSNIQMDVE 645  
QY 595 YLYPGGMGNRFRVSLKSYSGNY-----DLKYSDPKFAEIIITPPLSSNIQMDVE 645  
Db 585 -----SSRSPENPATYSASIAYTNTMTNASTYSTFAYAE-----SGPINLGIS 629  
QY 646 MOANSFQSDV-----NVLDKIEFLPSNTTTLBYEGERDLEKTKNAVNDLFTN 693  
Db 630 GSSRTFDISITKEAGANLYIDRIEIPVNTL---FEAEDLDVAKKAVNGLFTN 681

## RESULT 11

US-08-789-449-2  
; Sequence 2, Application US/08789449  
; Patent No. 5824878  
; GENERAL INFORMATION:  
; APPLICANT: Ohba, Michio  
; APPLICANT: Iwahana, Hidenori  
; APPLICANT: Sato, Reichi  
; APPLICANT: Suzuki, No. 5824878ukazu  
; APPLICANT: Ogiwara, Katsutoshi  
; APPLICANT: Sakanaka, Kazunobu

```
;
;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: 50C
; IMMEDIATE SOURCE:
; LIBRARY: lambdaGEM-11 library of L. Fonceerrada
; CLONE: 50C(b)
; US-08-315-468-4

Query Match          20.4%; Score 745; DB 1; Length 1169;
Best Local Similarity 29.4%; Pred. No. 1.1e-36;
Matches 217; Conservative 142; Mismatches 274; Indels 104; Gaps 31;

QY  4 MSPYQNKNEYEILLES--SSNNTNTPNRYPPAN--NRDMSTMWDCOGIS-----W 50
Db  1 MSP-NQNEYEIIDATPSTSVSDNSNRYPPANEPFNALQNMKYDKLKMAGNVSEYPGS 59

QY  51 DEIWESVETITSGINLIEFVIE-----PSLGGINTLLS-IIGKLIPTNRQTVSALSICDL 105
Db  60 PEVFLSEQDAVKAADIVGKLLTGLGVFPVPIVSLVTLQIDILWPSKQKSQWEIPEQV 119

QY  106 LSIIRKEVADSVLSDAIDFDGKLNRYEYLSYLGAWLKD----GKPLQKTNNSDGLQVL 162
Db  120 EELNQIAIYARKALKSELEGIGNY-QLYLTALKEWKENPNNGSRLARDVRNR----- 172

QY  163 YPFKLSERDPNEITLGSLSRNNQAVLLLPFAQAAVQLLLLRDAVQYKAQMPPELSAEN 222
Db  173 --FEILDSLFTQYM-PSFRVTFNEVPFLVYVTAANLHLLLRDAISIFGEW--GLSTST 227

QY  223 VRSELISPNSGCDFTGDYVERLCKTAETNYCLYQVGLNQIKOGGTGADTWSKFNKF 282
Db  228 I-----NNYNNRQMKLTAEYSDHCVKWYETGLAKLK--GSSAKQWIDYNQF 271

QY  283 RREMTLAVLDIIAIFPTYPEKYPPLTHVELTREIYTDVAGYSS--GTYSWLRNWNFTN 340
Db  272 RREMTLVLVDVALFNSYDTRTYPLATTAQLTREVTDPGLGAVDVPNIGSWYDKAP-SFS 330

QY  341 GLEANGTRGCLVTWLSKIGIYNEYSV---RYFAGWVGTRHYEDYTKNGIFORMSGTT 396
Db  331 EIEKAARPHVFDYITGLTVYTKRSFTSDRMYRWYAGHQISYKHIGTSIFQMYGTN 390

QY  397 SN--DLRNIIDFQNAVYKITS--LAIMNLVGETTARPEYRVSKADFRYVG-----GPDLN 447
Db  391 QNLQSTSNFDTNYDIYKTLNSGAVLLDIVPGYTVTFPGMPETEPFMVNLNTRKTLT 450

QY  448 YDAGNGLSRMTIESTFPLVHLSNG---VRGPHRLSNAACVYVGNR---VNVYQWHTT 501
Db  451 YKPASKDIIDTRDSELELPETSGQPNFYESYSHRLGHIT-FYSSSTSTYVPVFSWTHR 509

QY  502 SLKRENIIBANOITQIPAVKSYVQLYANAYTVVIKGT-HTGGDLIRFLRT--KSEYNA 558
Db  510 SADLTWVSGEITQIPGKKSSTI-----GRNTYIINGRGYITGGDLVALTDRIGSCFOM 564

QY  559 VYAGCGIRLIINNKTAGQSYRIRFRYAADKAAFFSVLYPGGWSNRFVLSKSYSG-NY 617
Db  565 IF-----PESQRFIRIRYASNETSYISLY----GLNQSGTLKFNQTSYKNKE 608

QY  618 DDLKYSDFKPAEIIITPLPSSNIQMDVEHQANSFQSDVNV-VLDKIEFLPSNTTLLYERG 676
Db  609 NDLTYNDFKYIEY--PRVISVNASSNIQRLSIGIQTNTNLFIIDRIEFIPVDET---YEA 663

QY  677 ERLEKTKQAVNDLFTN 693
Db  664 ETDLEAKKAVNALFTN 680
```

RESULT 9

US-07-915-203-2

; Sequence 2, Application US/07915203

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; Patent No. 5359048
; GENERAL INFORMATION:
; APPLICANT: Onba, Michio
; APPLICANT: Iwahana, Hidenori
; APPLICANT: Sato, Reichi
; APPLICANT: Suzuki, No. 535904Bukazu
; APPLICANT: Ogiwara, Katsutoshi
; APPLICANT: Sakanaka, Kazunobu
; APPLICANT: Hori, Hidetaki
; APPLICANT: Aeano, Shouji
; APPLICANT: Kawasugi, Tadaaki
; TITLE OF INVENTION: No. 5359048el Microorganism and Insecticide
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/915,203
; FILING DATE: 19920723
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/K 301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1149 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-915-203-2
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Query Match          19.9%; Score 728.5; DB 1; Length 1149;
Best Local Similarity 29.9%; Pred. No. 3.2e-55;
Matches 232; Conservative 124; Mismatches 240; Indels 179; Gaps 34;

QY  4 MSPYQNKNEYEILLESNNNTNTPN--RYFPANNRDMSTMWDCOGISWDE----- 52
Db  1 MSP-NQNEYEIIDALSPSTSVSDNISRYPLANDQNTLNQNMKYDKLKMTESTNAELSRN 59

QY  53 --IWESVETITSGINLIEFVIE-----PSLGGINTLL--SIIGKLIPTNRQTVSALSICDL 105
Db  60 PCTFISAQDAVCTGDIVSTIISGIGIPVLGEVFSILGSLGLLWPSNNENWQIPMNRV 119

QY  106 LSIIRKEVADSVLSDAIDFDGKLNRY--EYIISYLGAWLKQKPLQKTNNSDGLQVL 162
Db  120 EELIDQKILDSVRSRAIAD---LANSRIAVEYVQNALEDWRKNP---HSTRSAAL---- 168

QY  163 YPFKLSERDPN--EITLG---GSLSRNNAQVLLLPFAQAAVQLLLLRDAVQYKAQMPFF 217
Db  169 ----VKERFGNAEALRTNMGFSQTNVETPLLPYQAASLHLLVMRDVQIYKQEW-- 222

QY  218 LSAENVRELISPNSGCDFTGDIYVERLCKTAETNYCLYQVGLNQIKOGGTGADTWS 277
Db  223 -----YFQNDIDL---FYKEQVSYTARYSDHCQVYNAGLNKLR--GTGAKQWV 266

QY  278 KPNKFRREMTLAVLDIIAIFPTYPEKYPPLTHVELTREIYTDVAG--YSSGYSWLRNMP 336
Db  267 DYNRRFRREMNVMVLDLVALFPNYDARIYPLETNAELTREIFDTPVGSYVYTGQSSTLISWY 326

QY  337 N-----TFNGLEANGTRGCLVTWLSKIGIYNEY----VSRYPAGWVGTRHYEDYTKG 385
```





```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1156 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-002-285-70

Query Match          20.4%; Score 747; DB 2; Length 1156;
Best Local Similarity 30.6%; Pred No. 7,3e-57;
Matches 230; Conservative 130; Mismatches 249; Indels 142; Gaps 31;

QY 9 NKNYEILESSNNNTNPN--RYPPANNRDMSTMWNCQCG---ISW-DEIWESVETITS 62
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 NONKHGIIGASCGCASDDVAKYPLANNPYSSALNLSQNSILLNWINIIGDAAKEAVS 61
QY 63 IGINLIEFVIEPSLGG-INTLLSIIGKLI-PTNRQTVSALSICDLSLIRKEVADSVLSD 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 IGTITVSLITAPSLTGLISIVYDLIGKVLGGSSQGSISDLSICDLSLIDLRVSQSVLND 121
QY 121 AIADFDGKLNKRYEYLSYLGAWLKDGKPLQKTNNSDIGLVYVFKLSERDFNEIL---- 176
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
122 GIADFNGLVLYRN-YLEALDSWKN-----PNSASAEELTRPRIADSEFDRLTRGS 174
QY 177 ---GGSLSRNNAQVLLPTFAQANVQLLLLRDAVQYKAQW-----FPFLSAENVRSBLI 228
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
175 LTNGGSLARNAQVILLPSFASAFFHLLLRDATRYGTNMGLYNATPFINYQSKLVLI 234
QY 229 SPNSGCDFTGDIYERLCKTAEYTYNCLYQVGLNQIKQGTGADTWSKKNKPREMTL 288
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
235 E-----LYTDCVHWYNRGNFELRQRTSATAWLEFHRYREMTL 274
QY 289 AVLDDIIAIFTPTDFEYKPLPHTHVELTREIYTDVAGY-----SSGTYSWLR--NWPNTFNGL 342
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
275 MWLDIVASFSSLDIINYPIETDFQLSRVIYTDPIGFVIRSSLRGSWFSFVNRA--FSDL 333
QY 343 EANGTRGPGVLTWLSKIGIYNEVYSRYFAG-----WVGTRHYEDYTKGNGIFORMSGT 395
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
334 E-NAIPNRPSPFLNMIISTGSLTPVSPSTDRARVWYGSRDRI SPANSPQITELISGQ 392
QY 396 TSNDLRNIDFQADVYKITSALMILVGETTARPEYRSKADFRVGGPDLDYAGNGL 455
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
393 HTTATQTILGRN--IFRVDSSQA--CNL-NDTT----YGVNRAVF-----YHDASEGS 435
QY 456 SRMTIESTFPLVLHSHNGVRGP-----SHRLSNAACVVYV----- 489
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
436 QBSVVEG-----YIRTGIDNPRVQNTIYLPQNSDIPEDYTHILSTINLTGGLRQV 491
QY 490 ----NSRVNVYGWTHSLKRENIIBANOITQIPAVKSYLQNLANAYTVYIKGTHTCGD 545
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
492 ASNRSSSLVMYGWTHSKLARNTNIPDRITQIPLTK----VDTRGTGVSVDNPGFIGA 547
QY 546 LIRPLRTKSEYNAVAGGIRLIINNKTAGOSYRIRFPYAADKAFFSVLYPGWGNR 605
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
548 LLQ-----RTDHGSL-----GVLRVQFPLHLRQOYRIRVYASTNIRLSV-----NGS 591
QY 606 FVSLSKSYSGNY---DDLKYSDFKAEIITPPLP--SSNIQMDVEMQANSFQSDVNVVLDK 661
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
592 FGTISQNLPSWTRWLEDLYGSAFRENTSRPTASPDQIRLTETPSFIRQEVV--DR 649
QY 662 IEFLPSNTTTLLEYGERDLEKTKNAVNDLFT 692
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
650 IEFIPVNPTR---EAKEDLEAAKAVASLFT 677
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RESULT 5

US-09-589-477-70

; Sequence 70, Application US/09589477

; Patent No. 6570005

```
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stockhoff, Brian
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/589,477
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1156 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-589-477-70
```

```
Query Match          20.4%; Score 747; DB 2; Length 1156;
Best Local Similarity 30.6%; Pred No. 7,3e-57;
Matches 230; Conservative 130; Mismatches 249; Indels 142; Gaps 31;

QY 9 NKNYEILESSNNNTNPN--RYPPANNRDMSTMWNCQCG---ISW-DEIWESVETITS 62
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 NONKHGIIGASCGCASDDVAKYPLANNPYSSALNLSQNSILLNWINIIGDAAKEAVS 61
QY 63 IGINLIEFVIEPSLGG-INTLLSIIGKLI-PTNRQTVSALSICDLSLIRKEVADSVLSD 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 IGTITVSLITAPSLTGLISIVYDLIGKVLGGSSQGSISDLSICDLSLIDLRVSQSVLND 121
QY 121 AIADFDGKLNKRYEYLSYLGAWLKDGKPLQKTNNSDIGLVYVFKLSERDFNEIL---- 176
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
122 GIADFNGLVLYRN-YLEALDSWKN-----PNSASAEELTRPRIADSEFDRLTRGS 174
QY 177 ---GGSLSRNNAQVLLPTFAQANVQLLLLRDAVQYKAQW-----FPFLSAENVRSBLI 228
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
175 LTNGGSLARNAQVILLPSFASAFFHLLLRDATRYGTNMGLYNATPFINYQSKLVLI 234
QY 229 SPNSGCDFTGDIYERLCKTAEYTYNCLYQVGLNQIKQGTGADTWSKKNKPREMTL 288
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
235 E-----LYTDCVHWYNRGNFELRQRTSATAWLEFHRYREMTL 274
QY 289 AVLDDIIAIFTPTDFEYKPLPHTHVELTREIYTDVAGY-----SSGTYSWLR--NWPNTFNGL 342
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Db 598 GGQSVNMPLQKMEIGENLTSTRFYTRDFSNPFSFRANPDI--IGISEQPLFGAGSISS 655  
Qy 654 DVNVVLDDKIEFLPSNTTILEYEGERDLKTKNAVNDLFTN 693  
Db 656 G-BLYIDKIEIILADAT---FEAESDLERAQKAVNALFTS 691

## RESULT 3

US-09-001-982-10  
; Sequence 10, Application US/09001982  
; Patent No. 6204246  
; GENERAL INFORMATION:  
; APPLICANT: Bosch, Hendrick J.  
; APPLICANT: Stiekema, Willem J.  
; TITLE OF INVENTION: Hybrid Toxin  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6204246artis Corporation  
; STREET: 3054 Cornwalleis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patencin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/001,982  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/602,737  
; FILING DATE: 21-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1156 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-001-982-10

Query Match 20.4%; Score 747; DB 2; Length 1156;  
Best Local Similarity 30.6%; Pred. No. 7.3e-57;  
Matches 230; Conservative 130; Mismatches 249; Indels 142; Gaps 31;

Qy 9 NKNEYELSSNNNTNPN--RYPANNRDMSTMNDCCG---ISW-DEIVESVETIS 62  
Db 2 NQNKHGIISGSCGASDDVADKPLANNPYSSALNLSNCSILNINIIGDAAKEAVS 61  
Qy 63 IGINLIEFVIEPSLGG-INTLSIIIGKLI-PNTRQTVSALSICDLISIRKEVADSVLSD 120  
Db 62 IGTIVSLITAFSLTGLISIVVDLICKVLGGSGQISDLSICDLLSIIDLVSQSVLND 121  
Qy 121 ATADPGKLNTRYVLSYLGAWLKDGKPLQKTNNSDGLVYVFKLSERDFNEIL---- 176  
Db 122 GIADFNGSVLLYRN-YLEALDSNKN-----PNSASAEELRTRFRADSEDFRILTRGS 174  
Qy 177 ---GGSLRNNAQVILLPTFAOANVQLLLLDVAVQYKAQW-----FPFLSAENVRSLEI 228  
Db 175 LTVNGSLAQNAQILLPSFASAPFHLULLLDKDATRYGNWGLYNATPINTQSKLVELI 234  
Qy 229 SPNSGCDFTGDYERLKCKTASEYTNCLYVYQVGLNQIKQGGTGADTWSKFNKFRREMTL 288  
Db 235 E-----LYTDYCVHWYNRGNFELRQRTGSATAWLEFHYRREMTL 274

Qy 289 AVLDDIATPTDYFEKYPPLPHTVELTREIYTDVGY-----SSGTYSWHLR--NHPNTNGL 342  
Db 275 MVLDIVASFSSLDITNYPIETDFQLSRVIYTDPIGFVHRSSLRGESWFSFVNRA--FSDL 333  
Qy 343 EANGTRGPGLVTLWSKIGIYNEVSVRFAG-----WVGTIRHYEDYTKNGIGIFORMSGT 395  
Db 334 E-NAIENPRPSWFLNMIISTGSLTLPVSPSTDRARVWYGSRRDIRSPANSQFTTELISGQ 392  
Qy 396 TSNLNRIDFQNAVYKITSLAIMNLVGETTARPEYRVSKADFRVVGPDNLNDAGNGL 455  
Db 393 HTTATQTILGRN--IPRVDSQA--CNL-NDTT-----YGVNRAVF-----YHDASEGS 435  
Qy 456 SRMTIESTFPLVLHNSGVGRP-----SHRLSNAACVVYVY-----489  
Db 436 QRSVYEG---YIRTTGIDNPRVQNTIYLPGENSDIPTPDYTHILSTTINLTGSLRQV 491  
Qy 490 ----NSRVNVYGTWHTSLKRENIIEANQITQIPAVKSYVLQNYLANAYTVIKGTHGGD 545  
Db 492 ASNRSSLVMYGWTSHKSLARNNTINPRITQIPLTK-----VDRGTGVSIVNDPFGFIGGA 547  
Qy 546 LIRFLRTKSEYNAVYAGGIRLIINNKTAGQSYRIFRYAADKAAPFVSVLYPGMGSNR 605  
Db 548 LLQ-----RTDHGSL---GVLRVQPLHLRQQVIRVRVASTTNIRLSV-----NGS 591  
Qy 606 FVSLEKSYSGNY---DDLKYSDFKFAEITPPLP--SSNTQMOMVEMQANSFQSDVNVVLDK 661  
Db 592 FGTISQNLFPSTWRLGEDLYGSAIFRENTSIRPTASPDQIRLTIEPFIQEVYV--DR 649  
Qy 662 IEFPLSNTTILEVEGERDLEKTKNAVNDLFT 692  
Db 650 IEFIPVNPTR---EAKEDLEAAKAVASLFT 677

## RESULT 4

US-09-002-285-70  
; Sequence 70, Application US/09002285  
; Patent No. 6369213  
; GENERAL INFORMATION:  
; APPLICANT: Schnepf, H. Ernest  
; APPLICANT: Wicker, Carol  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Walz, Michelle  
; APPLICANT: Stockhoff, Brian  
; APPLICANT: Muller-Cohn, Judy  
; TITLE OF INVENTION: Toxins Active Against Pests  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/002,285  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/886,615  
; FILING DATE: 1-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/674,002  
; FILING DATE: 1-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sanders, Jay M.  
; REGISTRATION NUMBER: 39,355  
; REFERENCE/DOCKET NUMBER: MA-701C2

63 IGINLIEFVIEPSLGG-INTLLSIIGKLI-PTNRQTVSALSICDLSIIRKEVADSVLSD 120  
62 IGTIVSLTAPSLTGLISIVYDLIGKVLGGSSQGISDLSICDLSIIDURVQSGLND 121  
121 AIADPDGKLNRYEYLSYLGAWLKGPKLQKTNNSDIGQVYVYFKLSERDFNEIL---- 176  
122 GIADFNGLVLYRN-YLEALDSWKN-----PNSASAEELRTRFRIADSEFDRILTRGS 174  
177 ---GGSLSRNAQVLLPTFAQAAVQLLLLDADAVQYKAQW-----PFLSAENVRSBLI 228  
175 LTNGGSLARQNAQIILLPSFASAAFFHLLLRDADATRYGTNMGLYNATPFINYQSKLVELI 234  
229 SPNSGCDPTGDYERLCKTAEYNYCLYVQVGLNOIKQGTGADTWSKFNKPRREMTL 288  
235 E-----LYTDYCVHWYNRGNELRQRTSATWLEFHYRREMTL 274  
289 AVLDIIAIFPTDYFEKYPPLTHVELTRIYTDVAGY-----SSGTYSWLR--NWPNTFNGL 342  
275 MVLDIVASFSSLDITNYPIETDFQLSRVIYTDPIGFVHRSSLRGESWFSFVNRRAN-PSDL 333  
343 EANGTRGPGCLVTWLSKIGIYNEYSRYFAG-----WVGTRHYEDYTKNGIFORMSGT 395  
334 E-NAIPNPRPSWFLNNMIISTGLTLPVSPSTDRARVWYGSRRDRISPANSQFITELSGQ 392  
396 TSNDLRNIDFONADVYKITSIAIMNLVGETTARPEYRVSKADFRVRGPGDLNVDAGNGL 455  
393 HTTATQTILGRN--IFRVDQA-CNL-NDTT-----YGVNRAVF-----YHDASEGS 435  
456 SRMTIESTPPLVLHNSGVGRP-----SHRLSNAACVVYVY----- 489  
436 QRSVYEG---YIRTTGIDNPRVQNTYLPGENSDIPTPEDYTHILSTTLNLTGGLRQV 491  
490 ---NSRVNYGVWTHSLKRENIIEANQITQIPAKSYLYQLYLANATYVIKGT-HTGG 544  
492 ASNRSSSLVYMWGTHKSLARNNTINPDRIQTQPLVKGRVW-----GGTSVITGPGFTGG 546  
545 DLIRFLRTKSEYNVAVAGGIRLIIN-NKTAGQSVRIIRFVAAADKAFFSVLYPGGWS 603  
547 DILR-----RNTF-----GDFVSLQVNIINSPIQRLFRFRYASSRDARVILVTGAASGV 597  
604 NRVFLEKSYSNGYD-----DLKYSDFK--FAEITPPLPSSNIQMDVEMQANSFQS 653  
598 GQGVSNVPLQKTMIEGNLTSRTYTDPSNPFSPFRANPDI--IGISEQPLFGAGSISS 655  
654 DVNVVLDKIEPLSPNTTILEYGERDLEKTKNAVNDLFTN 693  
656 G-ELYDKIEITLADAT---FEASDLERAQKAVNALETS 691

## RESULT 2

US-09-668-650-12

; Sequence 12, Application US/09668650

; Patent No. 6780408

; GENERAL INFORMATION:

; APPLICANT: Bosch, Hendrick J.

; TITLE OF INVENTION: Hybrid Toxin

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSER: No. 6780408artis Corporation

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: NC

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/668,650

; FILING DATE: 22-Sep-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/001,982  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/602,737  
; FILING DATE: 21-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1242 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-668-650-12

Query Match 20.9%; Score 762.5; DB 2; Length 1242;

Best Local Similarity 31.2%; Pred. No. 3.4e-58;

Matches 237; Conservative 126; Mismatches 252; Indels 145; Gaps 33;

QY 9 NKNYEILESSNNNTNPN--RYPPANNRDMSTMSWDCQ---ISW-DETWESVETITS 62  
DB 2 NQKHGIIGASCACDDVAKYPLANNPYSSALNLSQNSSSILNWINIIGDAKEAVS 61  
QY 63 IGINLIEFVIEPSLGG-INTLLSIIGKLI-PTNRQTVSALSICDLSIIRKEVADSVLSD 120  
DB 62 IGTIVSLTAPSLTGLISIVYDLIGKVLGGSSQGISDLSICDLSIIDURVQSGLND 121  
QY 121 AIADPDGKLNRYEYLSYLGAWLKGPKLQKTNNSDIGQVYVYFKLSERDFNEIL---- 176  
DB 122 GIADFNGLVLYRN-YLEALDSWKN-----PNSASAEELRTRFRIADSEFDRILTRGS 174  
QY 177 ---GGSLSRNAQVLLPTFAQAAVQLLLLDADAVQYKAQW-----PFLSAENVRSBLI 228  
DB 175 LTNGGSLARQNAQIILLPSFASAAFFHLLLRDADATRYGTNMGLYNATPFINYQSKLVELI 234  
QY 229 SPNSGCDPTGDYERLCKTAEYNYCLYVQVGLNOIKQGTGADTWSKFNKPRREMTL 288  
DB 235 E-----LYTDYCVHWYNRGNELRQRTSATWLEFHYRREMTL 274  
QY 289 AVLDIIAIFPTDYFEKYPPLTHVELTRIYTDVAGY-----SSGTYSWLR--NWPNTFNGL 342  
DB 275 MVLDIVASFSSLDITNYPIETDFQLSRVIYTDPIGFVHRSSLRGESWFSFVNRRAN-PSDL 333  
QY 343 EANGTRGPGCLVTWLSKIGIYNEYSRYFAG-----WVGTRHYEDYTKNGIFORMSGT 395  
DB 334 E-NAIPNPRPSWFLNNMIISTGLTLPVSPSTDRARVWYGSRRDRISPANSQFITELSGQ 392  
QY 396 TSNDLRNIDFONADVYKITSIAIMNLVGETTARPEYRVSKADFRVRGPGDLNVDAGNGL 455  
DB 393 HTTATQTILGRN--IFRVDQA-CNL-NDTT-----YGVNRAVF-----YHDASEGS 435  
QY 456 SRMTIESTPPLVLHNSGVGRP-----SHRLSNAACVVYVY----- 489  
DB 436 QRSVYEG---YIRTTGIDNPRVQNTYLPGENSDIPTPEDYTHILSTTLNLTGGLRQV 491  
QY 490 ---NSRVNYGVWTHSLKRENIIEANQITQIPAKSYLYQLYLANATYVIKGT-HTGG 544  
DB 492 ASNRSSSLVYMWGTHKSLARNNTINPDRIQTQPLVKGRVW-----GGTSVITGPGFTGG 546  
QY 545 DLIRFLRTKSEYNVAVAGGIRLIIN-NKTAGQSVRIIRFVAAADKAFFSVLYPGGWS 603  
DB 547 DILR-----RNTF-----GDFVSLQVNIINSPIQRLFRFRYASSRDARVILVTGAASGV 597  
QY 604 NRVFLEKSYSNGYD-----DLKYSDFK--FAEITPPLPSSNIQMDVEMQANSFQS 653  
DB 598 GQGVSNVPLQKTMIEGNLTSRTYTDPSNPFSPFRANPDI--IGISEQPLFGAGSISS 655



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QY 106 LSIIRKEVADSVLSDAIADFDGKLNRYEYLSYLGAWLKD-----GKPLQKTN 155
Db 120 EELINQKIAEYARNKALSEGLGNNY-QLYLTALBEEENPFRSRGFRSPALRDVRN 178
QY 156 SDIGQLVYFKLSERDFNEILGGSLSRNNAAVLLPFAQAANVQLLLRDAVOYKAQWF 215
Db 179 R-----FEILDSLFTQYM-PSFRVTNFEVPLTVVYMAAANLHLLKDAASIFGEW- 228
QY 216 PFLSAENVRSSELISPNSCDFT--GDYVERLKCKTAETNYCLYQVGLNQIKOGGTGA 273
Db 229 -----GWSTTTNNYDQMKLTAEYSDHCVKWTETGLAKLK--GTSA 269
QY 274 DTWSKFNFRREMTLAVLDIIAIPFYDEKYPPLTHVELTREIYTDVG--YSGTYSW 331
Db 270 KQWVDYNQFRREMTLAVLDVVALFPNYDTRTPMETKAQLTREYVTDPLGAVNVSSIGSW 329
QY 332 LRNPNTFNGLEANGTRGGLVTLWSKIGIYNEYVS---RYFAGWVQTR-HYEDYTKGN 386
Db 330 YDKAP-SFGVIESSVIRPPHVPDYITGLTVYQSRSSISSARYIRHWAGHOISYHRVSRGS 388
QY 387 GIFORMSGTTSN--DLRNIQFQADVYKITS--LAIMNLVGETTARPEYRVSKADFRVVG 442
Db 389 NL-QQMYGTGNLHSTSTFDFTNYDIYKTLSDAVLLDIV-----YPGY-----TYIFPG 437
QY 443 GPDLYNADGN-----NGLSRMTIESTF-----PLVLHSGVVRGSPSHLSNAA 484
Db 438 MPEVEFFWVQNLNTRKTLKYNPVSKDIIASTRDSLELPPETSQPNVESYSHRLCHIT 497
QY 485 CV-VYGNR--VNVYGTHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVYIKGT- 540
Db 498 SIPATGNTTGLVPVFSWTHRSADLNTIYSDKITQIPAVKCW--DNL---PFVPVVKGP 552
QY 541 HTGGDLIRFLRTKSEYNAYV-AGGGIRLIINNKTAGOSYRIRFRVAADKAAPFSVLYPG 599
Db 553 HTGGDLQYNRSTGSGVTLFLARYGLAL-----EKAGK-YRVLRYATDADIVLHV----- 602
QY 600 GWSNRFRVLSKYSYSGNYDDLKYSDPKFAEIIITPPLPSSN-----IQMDVEMQANSFQSDV 655
Db 603 ---NDAQIQMPKTNPG-EDLTSKTFKVADAITTVNLATDSSVAVKHNVDGDPNSTLSGI 658
QY 656 NVLDKIEFLPSNTTLEYEGE 677
Db 659 -VYVDRIEFIPVDET---YEAE 676

```

## RESULT 15

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US-11-108-389-40
; Sequence 40, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McQuichen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 40

```

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; LENGTH: 676
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-108-389-40

```

```

Query Match 18.1%; Score 660; DB 7; Length 676;
Best Local Similarity 29.1%; Pred. No. 4.2e-45;
Matches 216; Conservative 138; Mismatches 254; Indels 134; Gaps 37;

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QY 4 MSPONKNEYEILS--SSNNTNPNRYPPAN--NRDMSTMWNDCCQIS-----W 50
Db 1 MSP-NNQNEYEIIIDATPSTSVSNDNRYPPANETNALQNMNDYKDYLKASAGNASEYPGS 59
QY 51 DEIWESVETITSIGINLIEFVIE---PSLGGINTLLS-IIGKLIPTRQTVSALSICDL 105
Db 60 PEVLVSQDAAKAADIVGKLSGLGVFPVGPVLSLTQLDILWPSEKESQWEIFMEQV 119
QY 106 LSIIRKEVADSVLSDAIADFDGKLNRYEYLSYLGAWLKD-----GKPLQKTN 155
Db 120 EELINQKIAEYARNKALSEGLGNNY-QLYLTALBEEENPFRSRGFRSPALRDVRN 178
QY 156 SDIGQLVYFKLSERDFNEILGGSLSRNNAAVLLPFAQAANVQLLLRDAVOYKAQWF 215
Db 179 R-----FEILDSLFTQYM-PSFRVTNFEVPLTVVYMAAANLHLLKDAASIFGEW- 228
QY 216 PFLSAENVRSSELISPNSCDFT--GDYVERLKCKTAETNYCLYQVGLNQIKOGGTGA 273
Db 229 -----GWSTTTNNYDQMKLTAEYSDHCVKWTETGLAKLK--GTSA 269
QY 274 DTWSKFNFRREMTLAVLDIIAIPFYDEKYPPLTHVELTREIYTDVG--YSGTYSW 331
Db 270 KQWVDYNQFRREMTLAVLDVVALFPNYDTRTPMETKAQLTREYVTDPLGAVNVSSIGSW 329
QY 332 LRNPNTFNGLEANGTRGGLVTLWSKIGIYNEYVS---RYFAGWVQTR-HYEDYTKGN 386
Db 330 YDKAP-SFGVIESSVIRPPHVPDYITGLTVYQSRSSISSARYIRHWAGHOISYHRVSRGS 388
QY 387 GIFORMSGTTSN--DLRNIQFQADVYKITS--LAIMNLVGETTARPEYRVSKADFRVVG 442
Db 389 NL-QQMYGTGNLHSTSTFDFTNYDIYKTLSDAVLLDIV-----YPGY-----TYIFPG 437
QY 443 GPDLYNADGN-----NGLSRMTIESTF-----PLVLHSGVVRGSPSHLSNAA 484
Db 438 MPEVEFFWVQNLNTRKTLKYNPVSKDIIASTRDSLELPPETSQPNVESYSHRLCHIT 497
QY 485 CV-VYGNR--VNVYGTHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVYIKGT- 540
Db 498 SIPATGNTTGLVPVFSWTHRSADLNTIYSDKITQIPAVKCW--DNL---PFVPVVKGP 552
QY 541 HTGGDLIRFLRTKSEYNAYV-AGGGIRLIINNKTAGOSYRIRFRVAADKAAPFSVLYPG 599
Db 553 HTGGDLQYNRSTGSGVTLFLARYGLAL-----EKAGK-YRVLRYATDADIVLHV----- 602
QY 600 GWSNRFRVLSKYSYSGNYDDLKYSDPKFAEIIITPPLPSSN-----IQMDVEMQANSFQSDV 655
Db 603 ---NDAQIQMPKTNPG-EDLTSKTFKVADAITTVNLATDSSVAVKHNVDGDPNSTLSGI 658
QY 656 NVLDKIEFLPSNTTLEYEGE 677
Db 659 -VYVDRIEFIPVDET---YEAE 676

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Search completed: December 15, 2005, 11:21:11  
Job time : 14 secs

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Db 561 RSTGSGVTGLFLARYGLAL-----EKAGK-YRVLRYATDADIVLHV-----NDAQIOM 607
QY 610 EKSYSGNYDLKYSDFKFABIITPPLPSN-----IQMDVEMQANSFQSDVNVVLDKIEFL 665
Db 608 PKTMNPG-EDLTSKTFKVADAITTVNLATDSSVAVKHVNGEDPNSTLSGI-VYVDRIEFI 665
QY 666 PSNTTTLLEYEGE 677
Db 666 PVDET---YEAE 674

RESULT 13
US-11-108-389-50
; Sequence 50, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-108-389-50

Query Match 18.1%; Score 660; DB 7; Length 674;
Best Local Similarity 29.1%; Pred. No. 4.2e-45;
Matches 213; Conservative 141; Mismatches 262; Indels 116; Gaps 35;

QY 4 MSPYQNKNEVEILES--SSNNTNTPNRYEPAN--NRDMSTMWNDCQGIS-----W 50
Db 1 MSP-NNQNEYIIDAFTSTSVNSDNRNRYPPANEPTNALQNMDYKYLKMSAGNASEYPOS 59
QY 51 DEIWESVETITSGINLIEFVIE---PSLGGINTLLS-IIGKLIPTNRQTVSALSICDL 105
Db 60 PEVLVSGQDAAKAADIIVGKLLSGLVFPVGPVIVSLYTLQILILWPSEKQSWEIFMEQV 119
QY 106 LSIIRKEVADSVLSDAIADPDGKLKNRYBYIYSLGAWLKDGKPLQKTNNSDIGQLVYVF 165
Db 120 EELNQKIAEYARNKALSELEGLNNY-QLYLTALBEEENPNRFRSRQALRDVRNRF 178
QY 166 KLSERDFNEILGSLSRNNAQVLLPTFAQANVOLLILRLDADAVQYKAQWFPFLSAENVRS 225
Db 179 EILDSLFTQYM-PSFRVTVTFEVPFLTVYAMAANLHLLLKDASIFGEW----- 226
QY 226 ELISPNSGCDFT--GDYVERLCKTAETYNCLYWYQVGLNOLKGGTGAADTWSKFNKPR 283
Db 227 -----GWSTTINNYDRQMKLTAEYSDHCWKWETGLAKL-K-GTSAKQWVDYNQPR 277
QY 284 REMTLAVLDIIAIFPDYDEKYPPLPHTBELTREIYTDVAG--YSGTYSWLNRPNTFNG 341
Db 278 REMTLAVLDVAFNPDYTRTYPMETKAQLTREYTDPLGAVNVNNSIGSWYDKAP-SFGV 336
QY 342 LEANGTRGPGLVTLWLSKIGIYNEVVS---RYFAGWVGTR-HYEDYTKNGIFQRMSTTT 396
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Db 337 ISSSVIRPPHVDYITGLTVYITQSRSSISSARYIRHWAGHOISYHRVSRGSNL-QQMYGTN 395
QY 397 SN--DLRNIDFQADVYKITS--LAIMNLVGETTARPEYRVSKADPRRGGPDPLNTDAGN 452
Db 396 QNLHSTSTFDFTNYDIYKTLSDAVLLDIV-----YPGY-----TVIFFGMEPEVFMVN 445
QY 453 -----NGLSRMTIESTF-----PLVLHSGVGRGSPSHRSLUSNAACV-VYGNR- 492
Db 446 QLNNTKRTLKYNPVSXKDIIASTRDSLELPPEPSTSDQPNYESYSHRLCHITSIPATGNTTG 505
QY 493 -VNVYGWHTSLKRENIIEANOITQIPAVKSYVLQNYLANAYTYVIKGT-HTCGDLIRFL 550
Db 506 LVPFVSWTHRSADLNNIYSDKITQIPAVKCM--DNL-----PFPVVKGPGHTGGDLLQVN 560
QY 551 RTKSEYNNAVY-AGGGIRLIINNKTAGQSRYIRFRYAADKAAPFVSVLYPFGMGSRNFVSL 609
Db 561 RSTGSGVTGLFLARYGLAL-----EKAGK-YRVLRYATDADIVLHV-----NDAQIOM 607
QY 610 EKSYSGNYDDLKYSDFKFABIITPPLPSN-----IQMDVEMQANSFQSDVNVVLDKIEFL 665
Db 608 PKTMNPG-EDLTSKTFKVADAITTVNLATDSSVAVKHVNGEDPNSTLSGI-VYVDRIEFI 665
QY 666 PSNTTTLLEYEGE 677
Db 666 PVDET---YEAE 674

RESULT 14
US-11-058-727-40
; Sequence 40, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-058-727-40

Query Match 18.1%; Score 660; DB 7; Length 676;
Best Local Similarity 29.1%; Pred. No. 4.2e-45;
Matches 216; Conservative 138; Mismatches 254; Indels 134; Gaps 37;

QY 4 MSPYQNKNEVEILES--SSNNTNTPNRYEPAN--NRDMSTMWNDCQGIS-----W 50
Db 1 MSP-NNQNEYIIDAFTSTSVNSDNRNRYPPANEPTNALQNMDYKYLKMSAGNASEYPOS 59
QY 51 DEIWESVETITSGINLIEFVIE---PSLGGINTLLS-IIGKLIPTNRQTVSALSICDL 105
Db 60 PEVLVSGQDAAKAADIIVGKLLSGLVFPVGPVIVSLYTLQILILWPSEKQSWEIFMEQV 119
```

;; PRIOR APPLICATION NUMBER: 10/606,320  
;; PRIOR FILING DATE: 2003-06-25  
;; NUMBER OF SEQ ID NOS: 134  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 50  
;; LENGTH: 674  
;; TYPE: PRF  
;; ORGANISM: Bacillus thuringiensis (mutated)  
US-11-058-727-50

Query Match 18.1%; Score 660; DB 7; Length 674;  
Best Local Similarity 29.1%; Pred. No. 4.2e-45;  
Matches 213; Conservative 141; Mismatches 262; Indels 116; Gaps 35;  
QY 4 MSPYQNKVEYELLES--SSNNTNPNRYPPAN--NRDMSTMSWDCQGIS-----W 50  
DB 1 MSP-NQNEYELIDATPSTVSNSNRYPFANEPTNALQNDYKDYKMSAGNASEYPCS 59  
QY 51 DEIMESVETITSGINLIEFVIE----PSLGGINTLLS-IIGKLIPTNRQTVSALSICDL 105  
DB 60 PEVLVSGQDAAKAADIIVGKLLSGLGVFPVPIVSLYTLQILDLWPSGEKSQWEIFMEQV 119  
QY 106 LSIIRKEVADSVLSADIAFDGKLKNRYEYLSYLGAWLKDGKPLQKTNNSDIGOLVYVF 165  
DB 120 BELNQKIAEYARNKALSLEGLGNYY-QLYLTALKEEENPNRFRSRQALRDVNRNF 178  
QY 166 KLSERDFNEILGSLSRNNAQVLLPTFAQANVOLLRLDRDAVQYKAOWFPFLSAENVR 225  
DB 179 EILDSLFQYM-PSFRTVNFVFPFLTVYAMAANLHLLKASIFGEW----- 226  
QY 226 ELISPNSGCDFT--GDYERLCKTAETNYCLYVQVGLNQIKOGGTGADTWKFNKFR 283  
DB 227 -----GWSTTTINNYDROMKLTAEYSDHCWKVYETGLAKL-K-GTSAKQWVDYNQFR 277  
QY 284 REMTLAVLDIIAIPPTDYDEKYPPLTHVELTREIYTDVAG--YSSGTYSWLRNWPNTNG 341  
DB 278 REMTLAVLDVALLFPNYDRTYPMETKAQLTREVTYDPLGAVNVSSIGSWYDKAP-SFGV 336  
QY 342 LEANGTRGPGVLTWLSKIGIYNEVVS---RYFAGWVGR-HYEDYTKGNGIFQMSGTT 396  
DB 337 IESSVIRPPHVDYITGLTVYQSRISARIYHWAHQIYHVRVSGSNL-QQMYGTN 395  
QY 397 SN--DLRNIQFQADVYKITS--LAIMNLVGETTARPEYRVSKADFRVVGPDLDNYDAGN 452  
DB 396 QNLHSTSTFTDNYDIYKLSKDAVLLDIV-----YPGY-----TYIFPGMEVEFFMVN 445  
QY 453 -----NGLSRMTIESTF-----PLVLSHNGVRGSPHRLSNAACV-VYGNR- 492  
DB 446 QLNTRKTLKYNPVSQDIITASTRDSLELPETSDQPNYESYSHRLCHITSPATGNTTG 505  
QY 493 -VNVYGTWHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVIKGT-HTGGDLIRFL 550  
DB 506 LVPVSWTHRSADLNTIYSDKITQIPAVKCH--DNL-----PFVPVVGKPGHTGGDLQYN 560  
QY 551 RTKSEYNNAVY-AGGGIRLIINNKTAGQSYRIRFRYAADKAAFFSVLYPGGNGSRFVSL 609  
DB 561 RSTGSGVTGLFARYGLAL----EKAGK-YRVLRYATDADIVLHV-----NDAQIQM 607  
QY 610 EKSYSQNYDDLYSKDPKFAEITPPLPSSN-----TOMVEMQANSFQSDVNVVLKIEPL 665  
DB 608 PKTMNFG-BDLTSKTPKVAADAITVNLATDSSVAVKHNVGDPNPTLSGI-VYVDRIEPI 665  
QY 666 PSNTTLEVEGE 677  
DB 666 PVDET---YEAE 674

RESULT 12  
US-11-108-389-44  
;; Sequence 44, Application US/11108389  
;; Publication No. US20050261188A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Andre R. Abad

;; APPLICANT: Ronald D. Flannagan  
;; APPLICANT: Rafael Herxmann  
;; APPLICANT: Theodore W. Kahn  
;; APPLICANT: Albert L. Lu  
;; APPLICANT: Billy Fred McCutchen  
;; APPLICANT: James K. Presnail  
;; APPLICANT: James F.H. Wong  
;; APPLICANT: Cao-Guo Yu  
;; TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal  
;; TITLE OF INVENTION: Activity  
;; FILE REFERENCE: 35718/291049  
;; CURRENT APPLICATION NUMBER: US/11/108.389  
;; CURRENT FILING DATE: 2005-04-18  
;; PRIOR APPLICATION NUMBER: 60/391,786  
;; PRIOR FILING DATE: 2002-06-26  
;; PRIOR APPLICATION NUMBER: 60/460,787  
;; PRIOR FILING DATE: 2003-04-04  
;; PRIOR APPLICATION NUMBER: 10/606,320  
;; PRIOR FILING DATE: 2003-06-25  
;; NUMBER OF SEQ ID NOS: 134  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 44  
;; LENGTH: 674  
;; TYPE: PRF  
;; ORGANISM: Bacillus thuringiensis (mutated)  
US-11-108-389-44

Query Match 18.1%; Score 660; DB 7; Length 674;  
Best Local Similarity 29.1%; Pred. No. 4.2e-45;  
Matches 213; Conservative 141; Mismatches 262; Indels 116; Gaps 35;  
QY 4 MSPYQNKVEYELLES--SSNNTNPNRYPPAN--NRDMSTMSWDCQGIS-----W 50  
DB 1 MSP-NQNEYELIDATPSTVSNSNRYPFANEPTNALQNDYKDYKMSAGNASEYPCS 59  
QY 51 DEIMESVETITSGINLIEFVIE----PSLGGINTLLS-IIGKLIPTNRQTVSALSICDL 105  
DB 60 PEVLVSGQDAAKAADIIVGKLLSGLGVFPVPIVSLYTLQILDLWPSGEKSQWEIFMEQV 119  
QY 106 LSIIRKEVADSVLSADIAFDGKLKNRYEYLSYLGAWLKDGKPLQKTNNSDIGOLVYVF 165  
DB 120 BELNQKIAEYARNKALSLEGLGNYY-QLYLTALKEEENPNRFRSRQALRDVNRNF 178  
QY 166 KLSERDFNEILGSLSRNNAQVLLPTFAQANVOLLRLDRDAVQYKAOWFPFLSAENVR 225  
DB 179 EILDSLFQYM-PSFRTVNFVFPFLTVYAMAANLHLLKASIFGEW----- 226  
QY 226 ELISPNSGCDFT--GDYERLCKTAETNYCLYVQVGLNQIKOGGTGADTWKFNKFR 283  
DB 227 -----GWSTTTINNYDROMKLTAEYSDHCWKVYETGLAKL-K-GTSAKQWVDYNQFR 277  
QY 284 REMTLAVLDIIAIPPTDYDEKYPPLTHVELTREIYTDVAG--YSSGTYSWLRNWPNTNG 341  
DB 278 REMTLAVLDVALLFPNYDRTYPMETKAQLTREVTYDPLGAVNVSSIGSWYDKAP-SFGV 336  
QY 342 LEANGTRGPGVLTWLSKIGIYNEVVS---RYFAGWVGR-HYEDYTKGNGIFQMSGTT 396  
DB 337 IESSVIRPPHVDYITGLTVYQSRISARIYHWAHQIYHVRVSGSNL-QQMYGTN 395  
QY 397 SN--DLRNIQFQADVYKITS--LAIMNLVGETTARPEYRVSKADFRVVGPDLDNYDAGN 452  
DB 396 QNLHSTSTFTDNYDIYKLSKDAVLLDIV-----YPGY-----TYIFPGMEVEFFMVN 445  
QY 453 -----NGLSRMTIESTF-----PLVLSHNGVRGSPHRLSNAACV-VYGNR- 492  
DB 446 QLNTRKTLKYNPVSQDIITASTRDSLELPETSDQPNYESYSHRLCHITSPATGNTTG 505  
QY 493 -VNVYGTWHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVIKGT-HTGGDLIRFL 550  
DB 506 LVPVSWTHRSADLNTIYSDKITQIPAVKCH--DNL-----PFVPVVGKPGHTGGDLQYN 560  
QY 551 RTKSEYNNAVY-AGGGIRLIINNKTAGQSYRIRFRYAADKAAFFSVLYPGGNGSRFVSL 609  
DB 561 RSTGSGVTGLFARYGLAL----EKAGK-YRVLRYATDADIVLHV-----NDAQIQM 607  
QY 610 EKSYSQNYDDLYSKDPKFAEITPPLPSSN-----TOMVEMQANSFQSDVNVVLKIEPL 665  
DB 608 PKTMNFG-BDLTSKTPKVAADAITVNLATDSSVAVKHNVGDPNPTLSGI-VYVDRIEPI 665  
QY 666 PSNTTLEVEGE 677  
DB 666 PVDET---YEAE 674



```
US-11-058-727-46
; Sequence 46, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2003-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-058-727-46

Query Match      18.1%; Score 660.5; DB 7; Length 675;
Best Local Similarity 29.1%; Pred. No. 3.8e-45;
Matches 216; Conservative 138; Mismatches 254; Indels 133; Gaps 37;

QY 4 MSPYQNKNEYILES--SSNNTNTPNRYPFAN--NRDMSTMSWDCQGIS-----W 50
Db 1 MSP-NQNEYEIIDATPSTSVSDNSRYPFANEPTNALQNDYKDKLXMSAGNASEYPGS 59
QY 51 DEIWSEVETITSGINLIEFVIE-----PSLGGINTLLS-IIGKLIPTRQTVSALSICDL 105
Db 60 PEVLVSGQDAKAADIIVGKLLSGLGVFPVGVISVLTQLIDILWPSEKQSEWIFMEQV 119
QY 106 LSIIRKEVADSVLSDAIDFDCKLKNRYEYLSYLGAWLKD-----GKPLQKTNNS 156
Db 120 BELINQKIAYARNKALSEGLGNNY-QLYLTALEEWEENPNRSRFRGPAALRDVNR 178
QY 157 DIGQLVYFKLSERDFNEILGSLSRNNAQVLLPTFAQAAVQLLLLRDAVQYKAQWFP 216
Db 179 -----FEILDSLFTQYM-PSFRVTNFEVPLTVYAMAANLHLLLLKXASIFGEW-- 227
QY 217 FLAENVRSELISPNSCDFT--GDYERLCKTAEYTNCLYTYQVGLNQIKOGGTGAD 274
Db 228 -----GWSTTTINNYDRQMKLTAEYSDHCVKVYETGLAKLK--GTSAK 269
QY 275 TWSKKNKPRREMTLAVLDIIAIFPTVDEKPLPHVLTRELYTDVAG--YSSGTYSWL 332
Db 270 QNVDNQFREMTELVAVLDVFPNVDYTRTPMETKAQLTREYVTDPLGANNVSGISGY 329
QY 333 RNWPNTFNGLEANGTRGPGVLTWLSKIGIYNEYVS-----RYFAGVWGR-HYEDYTKNG 387
Db 330 DKAP-SFGVIESVIRPPHVDYITGLTYTQSRSSARYTRHWAGHQSIVHRVSRGN 388
QY 388 IFQMSGTTSN--LURNIDFQNAVYKITS--LAINLVGETTARPEYRVSKADPRRVGG 443
Db 389 L-QQMYGTQNQLHSTFTDFNTYDIYKTLSDKAVLLDIV-----YPGY-----TVIFPGM 437
QY 444 PDLNYDAGN-----NGLSRMTIESTF-----PLVHNSGVNRPSPHRLSNAC 485
Db 438 PEVEFMVQNLNTRKTLKYNPVSKDIIASTRDSLELPETSDQPNYESYHRLCHITS 497
QY 486 V-VYGNRSR--VNVYGWTHTSKRENIIEANQITQIPAVKSYYLQNLANAYTVIKGT-H 541
```

```
US-11-108-389-46
; Sequence 46, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-108-389-46

Query Match      18.1%; Score 660.5; DB 7; Length 675;
Best Local Similarity 29.1%; Pred. No. 3.8e-45;
Matches 216; Conservative 138; Mismatches 254; Indels 133; Gaps 37;

QY 4 MSPYQNKNEYILES--SSNNTNTPNRYPFAN--NRDMSTMSWDCQGIS-----W 50
Db 1 MSP-NQNEYEIIDATPSTSVSDNSRYPFANEPTNALQNDYKDKLXMSAGNASEYPGS 59
QY 51 DEIWSEVETITSGINLIEFVIE-----PSLGGINTLLS-IIGKLIPTRQTVSALSICDL 105
Db 60 PEVLVSGQDAKAADIIVGKLLSGLGVFPVGVISVLTQLIDILWPSEKQSEWIFMEQV 119
QY 106 LSIIRKEVADSVLSDAIDFDCKLKNRYEYLSYLGAWLKD-----GKPLQKTNNS 156
Db 120 BELINQKIAYARNKALSEGLGNNY-QLYLTALEEWEENPNRSRFRGPAALRDVNR 178
QY 157 DIGQLVYFKLSERDFNEILGSLSRNNAQVLLPTFAQAAVQLLLLRDAVQYKAQWFP 216
Db 179 -----FEILDSLFTQYM-PSFRVTNFEVPLTVYAMAANLHLLLLKXASIFGEW-- 227
QY 217 FLAENVRSELISPNSCDFT--GDYERLCKTAEYTNCLYTYQVGLNQIKOGGTGAD 274
Db 228 -----GWSTTTINNYDRQMKLTAEYSDHCVKVYETGLAKLK--GTSAK 269
```



```
Db 438 MVNQLNTRKTLKYNPVSKDIIASTRDSLELPETSDQNPVSYSHRLCHITSIPATGN 497
QY 491 SR--VNVYGVWTHSTLKRNIIEANQITQIPAVKSYLYQNYLANAYTVYIKGT-HTGGDLI 547
Db 498 TTGLVPVFWSTHRSADLNNTIYSDKITQIPAVKCM--DNL---PFPVVKPGHGTGGDL 552
QY 548 RFLRTKSEYNAVY-AGGGIRLIINNKTAGQSVYRIRFRAADKAAFPSSVLYPGWGSNRF 606
Db 553 QYNRSTGSGVTGLFLARYGLAL-----EKAGK-TRVRLRYATDADIVLHV-----NDAQ 599
QY 607 VLSKSYSGNYDDLYSDFKFAEIIITPPLSSNIQMDVEM-----QANSFQSDVNVV 658
Db 600 IQPKTMNPG-EDLTSKTFKVADAIT-----TLNLTADSSALKHNLGDPNSTLSGI-VY 653
QY 659 LDKIEFLPSNTTLEYEGE 677
Db 654 VDRIEPIVDET---YEAE 669

RESULT 5
US-11-058-727-12
; Sequence 12, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (truncated)
US-11-058-727-12

Query Match 18.1%; Score 660.5; DB 7; Length 669;
Best Local Similarity 29.2%; Pred. No. 3.8e-45;
Matches 216; Conservative 136; Mismatches 252; Indels 135; Gaps 38;

QY 4 MSPYONKNEYEILES--SNNTNTNRYFPAN--NRDMSTMSWDCQGIS-----W 50
Db 1 MSP-NNQNEYIHDATPSTSVSDNSRNPFPANPTNALQNMDDKYOLKMSAGNASEYFGS 59
QY 51 DRIWESVETITSGINLIEFVIE---PSLGGINTLLS-IIGKLIPTNRQTVSALSICDL 105
Db 60 PEVLVSGQDAKAAADIVKLSGLGVFPVGVISLYTQILIDLPWSGEKSWEIFMEQV 119
QY 106 LSIIRKEVADSVLSDAIDFDGKLKNRYEYLSYLGAWLK---GKPLQKTNNSDIGQLV 162
Db 120 EELINGKIAEYARNKALSELEGLNNY-QLYLTAEWEENPNNGSRALRDVNR----- 172
QY 163 YVFKLSERDFNIELGSLSRNNAQVLLPTFAQANVQLLIRDAVOYKAQWFFPLSABN 222
Db 173 --FEILDLSLTQYM-PSFRVTFVFPFLTVYAMAANHLHLKLDASIFGEEM----- 221
QY 223 VRSELISPNSGCDFT--GDYERLCKTAETNYCLYVYQVGLNQLKQGGTGADTWSKFN 280
```

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Db 222 -----GWSITTTNNYDRQMKLTAEYSDHCVKMYETGLAKLK--GTSQAKQVMDYN 269
QY 281 KFRREMTLAVLDIIAIFPTYPDEKYPLPHTHVELTREIYTDVAG--YSSGTYSWLRNWPNT 338
Db 270 QFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVYTDPLGAVNVVSSIGSWYDKAP-S 328
QY 339 FNGLEANTRCPGLVTLWSKIGIYNEYVS-----RYFAGVWGR-HYEDYTKNGNIGIFORMS 393
Db 329 FGVIESSVIRPHVFDYITGLTVYVTSRSISSARYIRHWAGHOISYHRVSRGSLN-QQMY 387
QY 394 GTTNS--DLRNIDFONADVYKITS--LAIMNLVGETTARPEYRVSKADPRRVGGPDLAND 449
Db 388 GTNQMLHSTSTFDFTNYDIYKLSKDAVLLDIV-----YPGY-----TYIFFGMEVEEFF 437
QY 450 AGN-----NGLSRMTIESTF-----PLVLHNSGVRGSPHRLSNAACV-VYGN 490
Db 438 MVNQLNTRKTLKYNPVSKDIIASTRDSLELPETSDQNPVSYSHRLCHITSIPATGN 497
QY 491 SR--VNVYGVWTHSTLKRNIIEANQITQIPAVKSYLYQNYLANAYTVYIKGT-HTGGDLI 547
Db 498 TTGLVPVFWSTHRSADLNNTIYSDKITQIPAVKCM--DNL---PFPVVKPGHGTGGDL 552
QY 548 RFLRTKSEYNAVY-AGGGIRLIINNKTAGQSVYRIRFRAADKAAFPSSVLYPGWGSNRF 606
Db 553 QYNRSTGSGVTGLFLARYGLAL-----EKAGK-TRVRLRYATDADIVLHV-----NDAQ 599
QY 607 VLSKSYSGNYDDLYSDFKFAEIIITPPLSSNIQMDVEM-----QANSFQSDVNVV 658
Db 600 IQPKTMNPG-EDLTSKTFKVADAIT-----TLNLTADSSALKHNLGDPNSTLSGI-VY 653
QY 659 LDKIEFLPSNTTLEYEGE 677
Db 654 VDRIEPIVDET---YEAE 669

RESULT 6
US-11-108-389-6
; Sequence 6, Application US/1108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Maize optimized Cry1218-1
US-11-108-389-6

Query Match 18.1%; Score 660.5; DB 7; Length 669;
Best Local Similarity 29.2%; Pred. No. 3.8e-45;
```

; TITLE OF INVENTION: poynucleotide encoding the same
; FILE REFERENCE: OP1335
; CURRENT APPLICATION NUMBER: US/11/091,643
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1316
; TYPE: PRT
; ORGANISM: Bacillus popilliae
US-11-091-643-4

Query Match 18.3%; Score 668; DB 7; Length 1316;
Best Local Similarity 31.1%; Pred. No. 2.5e-45;
Matches 232; Conservative 105; Mismatches 262; Indels 148; Gaps 35;

QY 8 QNKNEVEILESSNN-TNTNPNRYPPANRDM-----STMSWND-CQG-----IS 49
Db 33 QSGNEMQIIQPSSNALLYSPNKPYATDPNVIAEGGSYKNWLDCTGTGTRSPETAAS 92
QY 50 WDEIWESVETITSIGINLIEFVIEPSLGGINTILLSIIGKLIPTNRQTVSALSICDLSII 109
Db 93 KGAVSAAI-TISTGLGLGLGVPFASQIGAPYTFL--LNTLMPAS--NTQWEQFIAHVEELI 148
QY 110 RKEVADSVLSDAIDPDGKLNRYEYLSYLGAWLKDGPLOKTNNSDIGQLVYYPKLE 169
Db 149 NAKLTDHVRNSALTKLNG-LRNNIEIYNEALIVWKD-----PNNS-----KLKD 192
QY 170 RDNFELG-----GSLSRNAQVLLPTPAQAANVOLLLRDAVQYKAQW-FPFLS 219
Db 193 DVRSKFVGLNSQPEEYIPQKEGFEVQLTIYAQSANLHLLRDSLSYGASWGFAQAT 252
QY 220 AENVRSSELSPNSGCDFTGDYERLCKTAETNYCLYVYVGLNQIKOGGTGADTWKFP 279
Db 253 IDN-----NYNRQIRKTAEYANHCCTWTYQTLGRLQ--GTTASSWLSY 293
QY 280 NKFRREMTLAVLDIIAIFPTYDPEKYPPLTHVELTREIYTDVAGYSSGTVSWLRNPNTF 339
Db 294 HRFRREMTLVLDICALFSYNDARSYPLEVRGELTREIYTDVP--APGT-NMIDRAP-SF 349
QY 340 NGLANGTRGPGVLTWLSKIGIYNEYSVRYFAGWGTG-----HYEDYTKNGGIFORMSG 394
Db 350 ABTENLVIRAPRTVTWIS--GDLIVYTGRLY-CYTGNNNDYWAHRLDFLETNG--YRPEG 404
QY 395 TTSNDLRNID-----FQNAVYKITSLAIMN-----LVGETTARPEYRVSKADFRV 441
Db 405 PTYGSTINISRTDSIPMNSIDVYSTVTVTGSAWPTGGFVLGVASAR-----FFSKS 456
QY 442 GGPDLNVDAGNGLSRMTIESTPPLVHNGV-----RGPSHRLSNAACVYVG-NSRV 493
Db 457 PSTGL---LGERVYQNPVYFSSSTLTFNLPVGDQDPTTAADYSHKUSCITAPRTGLNGTV 513
QY 494 NVYGWTHTSKLRENIIEANQITQIPAVKSYLQNYLANAYTVYIKGT-HTGGDLIRFLRT 552
Db 514 PVFGYRSATVSRDNIIEPKITQIPAVKSNLDN-----CPVVRGTGTGGDWL----- 562
QY 553 KSEYNAYAGGGRILLINKKTAQSYRIRFRVAADKAAPFSVLYPGGWGNS-----RVV 607
Db 563 KTSYLSVFV-----LRTISSRAGQSYRIRVYAAAVDLIMSIV-----SNDPFIISKGI 610
QY 608 SLEKSYSGNVDDLKYSDKFAET-ITPPLPSSNIQMDVEMQANSFOSDVNVVLDKTEFLP 666
Db 611 SLTKSMPPLETVPYEAFAFPADPGVTTTATANKRTTFO-----FHTGGAAIIDRIEFVP 665
QY 667 SNTTILEYGERDLEKTKNAVNDLFTN 693
Db 666 IEGSLFEYETKQLEKAKAVNHLFTD 692

RESULT 4
US-11-058-727-6
; Sequence 6, Application US/11058727
; Publication NO. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Maize optimized Cry12Ib-1
US-11-058-727-6

Query Match 18.1%; Score 660.5; DB 7; Length 669;
Best Local Similarity 29.2%; Pred. No. 3.8e-45;
Matches 216; Conservative 136; Mismatches 252; Indels 135; Gaps 38;

QY 4 MSPYQNKYEILESS--SSNNTNTPNRYPPAN--NRDMSTMSWNDCCQGIS-----W 50
Db 1 MSP-NNQNEYELIIDATPSTSVNSDSNRYPFANPTNALQNDYKDKLMSAGNASEYPS 59
QY 51 DEIWESVETITSIGINLIEFVIE-----PSLGGINTLLS-IIGKLIPTNRQTVSALSICDL 105
Db 60 PEVLVSGQDAAKAADIVGKLLSGLGVPFVGPVIVSLYQLIDILWPSGKESQWEIFMEQV 119
QY 106 LSLIRKEVADSVLSDAIDPDGKLNRYEYLSYLGAWLKD---CKPLOKTNNSDIGQLV 162
Db 120 BELINQKIAEYARNKALSEGLEGLGNNY-QLYLTALBEEBENPNNGSRALDRVNR- 172
QY 163 YVFKLSERDFNEILGGSLSRNNQVLLPTPAQAANVOLLLRDAVQYKAQWFPFLSAEN 222
Db 173 --FEILDSLFTQYM-PSFRVTNFEVPLTVVYMAANLHLLLLKDAISIFGEW----- 221
QY 223 VRSELISPSGCDFT--GDYYERLCKTAETNYCLYQVGLNQIKOGGTGADTWKSN 280
Db 222 -----GWSSTTINNYDROMKLTABYSDHCVKVVETGLAKLK--GTSAKQWVDVN 269
QY 281 KFRREMTLAVLDIIAIFPTYDPEKYPPLTHVELTREIYTDVAG--YSSGTVSWLRNPNT 338
Db 270 QFRREMTLAVLDVVALFPNYDTRTPYMETKAQLTREVTYDPLGAVNVVSSIGSWDKAP-S 328
QY 339 FNGLEANGTRGPGVLTWLSKIGIYNEYVS---RYFAGWGTGTR-HYEDYTKNGGIFORMS 393
Db 329 FGVTESSVIRPFPVFDYITGLTVYTSQSRSSISSARIYHAGHQSIRHVRSGNSL-QQNY 387
QY 394 GTTGN--DLRNIIDFONADVYKITS--LAIMNLVGETTARPEYRVSKADFRRVGGPDLYND 449
Db 388 GTNQNLHSTSTFDFTNYDIYKLSKDAVLDDIV-----YPGY-----TVIFPGMEVEFF 437
QY 450 AGN-----NGLSRMTIESTF-----PLVTLHNGVGRGSHLSNAACV-VYGN 490

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QY 163 YVFKLSERDFNEILGSLSRNNAQVLLPTFAQANVOLLILRDVAVOYKQWFPFLSAEN 222
Db 173 --FEILDSLFTQYM-PSFRVTNFEVPLFTVYAMAANLHLLLDKADSIPEGEEW-----221
QY 223 VRSELISPNSGCDFT--GDYERLCKTAETNYCLYVQVGLNQIKOGGTGADTWSKFN 280
Db 222 -----GWSTTTINNYDRQMKLTAEYSDCHVKWYETGLAKLK--GTSAKQWVDYN 269
QY 281 KFRREMTLAVLDIIAIFPTDYDEKYPPLTHVELTREIYTDVAG--YSSGTYSWLRNWPNT 338
Db 270 QFRREMTLAVLDVAVLFPNYDTRTPMETKAQLTREVYTDPLGAVNVSSIGSWYDKAP-S 328
QY 339 ENGLEANGTRGPGVLTWLSKIGIYNEVVS---RYFAGWVCTR-HYEDYTKNGIFORMS 393
Db 329 FGVISSVIRPHVDFDIITGLTVYQTSRISARIYRHWAGHQISYHRVSRGSNL-QQMY 387
QY 394 GTTSN--DLRNIQFQADVYKITS--LAIMNLVGETTARPEYRVSKADFRVGGPDLNYD 449
Db 388 GTNQNLHSTSTFTDNYDIYKLSKDAVLDDIV-----YPGY-----TYIFFGMEVEVFF 437
QY 450 AGN-----NGLSRMTIESTF-----PLVLHNSGVGRGSPHRLSNAACV-VYGN 490
Db 438 MVNQLNTRKTLKYNPVSXKDIIASTRDSLELPPEPESYSHRLCHITSIPATGN 497
QY 491 SR--VNVYGVWTHSLKRENIIEANQITQIPAVKSYLYQLNLANAYTVYIKGT-HTGGDLI 547
Db 498 TTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKWC--DNL---PFVPVVGKPGHTGGDL 552
QY 548 RFLRTKSEYNAVY-AGGGIRLIINNKTAGOSYRIRFRYAADKAAFFSYLYPGWGSNRF 606
Db 553 QYNRSTGSGVGLFLARYGLAL-----EKAGK-YRVLRYATDADIVLHV-----NDAQ 599
QY 607 VSLEKSYGNYDDLYKSDPKFAEITPPLPSNIOQMDVEM-----QANSFQSDVNVV 658
Db 600 IQMPKTMNPG-EDLTSKTFKVADAIT---TLNLATDSSLALKNLGEDPNSTLSGI-VY 653
QY 659 LDKIEFLPSNTTLEVEGERDLEKTKNAVNDLFTN 693
Db 654 VDRIEFIPVDET---YEAQDLEAAKAVNALFTN 685

```

## RESULT 2

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US-11-108-389-2
; Sequence 2, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 357118/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis

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## US-11-108-389-2

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Query Match 19.5%; Score 713.5; DB 7; Length 1206;
Best Local Similarity 30.1%; Pred. No. 5.3e-49;
Matches 227; Conservative 137; Mismatches 256; Indels 135; Gaps 38;

QY 4 MSPYQNKNEVILLES--SSNNTNPNRYPPAN--NRDMSTMSWDCQGIS-----W 50
Db 1 MSP--NNQNEVEIIDATSTSVSDNSNRYPPANETNALQNDYDKLQMSAGNASEYPGS 59
QY 51 DEIWESVETITISIGINLIEFVIE----PSLGGINTLLS-IIGKLIPTNRQTVSALSICDL 105
Db 60 PEVLVSGQDAKAADIIVGKLLSGLVFVGPVLSVLTQLDILWPSEKSEKQWEIFMEQV 119
QY 106 LSITRKEVADSVLSDAIDAFDCKLKNRYREYLSYLGAWLKD---GKPLQTKNNSDIDGLV 162
Db 120 EELINQIAEYARNKALSELEGLGNNY-QLYLTAALEEENPNRSRALRDYRNR-----172
QY 163 YVFKLSERDFNEILGSLSRNNAQVLLPTFAQANVOLLILRDVAVOYKQWFPFLSAEN 222
Db 173 --FEILDSLFTQYM-PSFRVTNFEVPLFTVYAMAANLHLLLDKADSIPEGEEW-----221
QY 223 VRSELISPNSGCDFT--GDYERLCKTAETNYCLYVQVGLNQIKOGGTGADTWSKFN 280
Db 222 -----GWSTTTINNYDRQMKLTAEYSDCHVKWYETGLAKLK--GTSAKQWVDYN 269
QY 281 KFRREMTLAVLDIIAIFPTDYDEKYPPLTHVELTREIYTDVAG--YSSGTYSWLRNWPNT 338
Db 270 QFRREMTLAVLDVAVLFPNYDTRTPMETKAQLTREVYTDPLGAVNVSSIGSWYDKAP-S 328
QY 339 ENGLEANGTRGPGVLTWLSKIGIYNEVVS---RYFAGWVCTR-HYEDYTKNGIFORMS 393
Db 329 FGVISSVIRPHVDFDIITGLTVYQTSRISARIYRHWAGHQISYHRVSRGSNL-QQMY 387
QY 394 GTTSN--DLRNIQFQADVYKITS--LAIMNLVGETTARPEYRVSKADFRVGGPDLNYD 449
Db 388 GTNQNLHSTSTFTDNYDIYKLSKDAVLDDIV-----YPGY-----TYIFFGMEVEVFF 437
QY 450 AGN-----NGLSRMTIESTF-----PLVLHNSGVGRGSPHRLSNAACV-VYGN 490
Db 438 MVNQLNTRKTLKYNPVSXKDIIASTRDSLELPPEPESYSHRLCHITSIPATGN 497
QY 491 SR--VNVYGVWTHSLKRENIIEANQITQIPAVKSYLYQLNLANAYTVYIKGT-HTGGDLI 547
Db 498 TTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKWC--DNL---PFVPVVGKPGHTGGDL 552
QY 548 RFLRTKSEYNAVY-AGGGIRLIINNKTAGOSYRIRFRYAADKAAFFSYLYPGWGSNRF 606
Db 553 QYNRSTGSGVGLFLARYGLAL-----EKAGK-YRVLRYATDADIVLHV-----NDAQ 599
QY 607 VSLEKSYGNYDDLYKSDPKFAEITPPLPSNIOQMDVEM-----QANSFQSDVNVV 658
Db 600 IQMPKTMNPG-EDLTSKTFKVADAIT---TLNLATDSSLALKNLGEDPNSTLSGI-VY 653
QY 659 LDKIEFLPSNTTLEVEGERDLEKTKNAVNDLFTN 693
Db 654 VDRIEFIPVDET---YEAQDLEAAKAVNALFTN 685

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## RESULT 3

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US-11-091-643-4
; Sequence 4, Application US/11091643
; Publication No. US20050246789A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moriichi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2005, 11:12:01 ; Search time 12 Seconds  
(without alignments)  
388.934 Million cell updates/sec

Title: US-10-781-979-3

Perfect score: 3655

Sequence: 1 MKQSPYQNKNEYEILESSS.....YEGERLEKTKNAVDLFTN 693

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51463 seqs, 6734788 residues

Total number of hits satisfying chosen parameters: 51463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/PCR\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	713.5	19.5	1206	7	US-11-058-727-2
2	713.5	19.5	1206	7	US-11-058-727-2
3	668	18.3	1316	7	US-11-091-643-4
4	660.5	18.1	669	7	US-11-058-727-6
5	660.5	18.1	669	7	US-11-058-727-12
6	660.5	18.1	669	7	US-11-058-389-6
7	660.5	18.1	669	7	US-11-058-389-12
8	660.5	18.1	675	7	US-11-058-727-46
9	660.5	18.1	675	7	US-11-058-389-46
10	660	18.1	674	7	US-11-058-727-44
11	660	18.1	674	7	US-11-058-727-50
12	660	18.1	674	7	US-11-058-389-44
13	660	18.1	674	7	US-11-058-389-50
14	660	18.1	676	7	US-11-058-727-40
15	660	18.1	676	7	US-11-058-389-40
16	659.5	18.0	675	7	US-11-058-727-78
17	659.5	18.0	675	7	US-11-058-727-78
18	659	18.0	674	7	US-11-058-389-78
19	659	18.0	674	7	US-11-058-727-82
20	659	18.0	674	7	US-11-058-389-76
21	659	18.0	674	7	US-11-058-389-82
22	659	18.0	676	7	US-11-058-727-72
23	659	18.0	676	7	US-11-058-389-72
24	658.5	18.0	673	7	US-11-058-727-8
25	658.5	18.0	673	7	US-11-058-727-26

26	658.5	18.0	673	7	US-11-058-727-30	Sequence 30, Appl
27	658.5	18.0	673	7	US-11-058-727-34	Sequence 34, Appl
28	658.5	18.0	673	7	US-11-108-389-8	Sequence 8, Appl
29	658.5	18.0	673	7	US-11-108-389-26	Sequence 26, Appl
30	658.5	18.0	673	7	US-11-108-389-30	Sequence 30, Appl
31	658.5	18.0	673	7	US-11-108-389-34	Sequence 34, Appl
32	658.5	18.0	677	7	US-11-058-727-52	Sequence 52, Appl
33	658.5	18.0	677	7	US-11-108-389-52	Sequence 52, Appl
34	657.5	18.0	673	7	US-11-058-727-70	Sequence 70, Appl
35	657.5	18.0	673	7	US-11-108-389-70	Sequence 70, Appl
36	657.5	18.0	675	7	US-11-058-727-42	Sequence 42, Appl
37	657.5	18.0	675	7	US-11-058-727-48	Sequence 42, Appl
38	657.5	18.0	675	7	US-11-108-389-42	Sequence 48, Appl
39	657.5	18.0	675	7	US-11-108-389-48	Sequence 48, Appl
40	657.5	18.0	677	7	US-11-058-727-84	Sequence 84, Appl
41	657.5	18.0	677	7	US-11-108-389-84	Sequence 84, Appl
42	657.5	18.0	1210	7	US-11-058-727-4	Sequence 4, Appl
43	657.5	18.0	1210	7	US-11-108-389-4	Sequence 4, Appl
44	656.5	18.0	675	7	US-11-058-727-74	Sequence 74, Appl
45	656.5	18.0	675	7	US-11-058-727-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1  
US-11-058-727-2  
; Sequence 2, Application US/11058727  
; Publication NO. US20050261483A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Rafael Herrmann  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Albert L. Lu  
; APPLICANT: Billy Fred McCutchen  
; APPLICANT: James K. Presnail  
; APPLICANT: James F.H. Wong  
; APPLICANT: Cao-Guo Yu  
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal  
; TITLE OF INVENTION: Activity  
; FILE REFERENCE: 35718/287809  
; CURRENT APPLICATION NUMBER: US/11/058,727  
; CURRENT FILING DATE: 2005-02-15  
; PRIOR APPLICATION NUMBER: 60/391,786  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: 60/460,787  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 10/606,320  
; PRIOR FILING DATE: 2003-06-25  
; NUMBER OF SEQ ID NOS: 134  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-11-058-727-2

Query Match	19.5%	Score 713.5;	DB 7;	Length 1206;
Best Local Similarity	30.1%	Pred. No. 5.3e-49;		
Matches 227;	Conservative 137;	Mismatches 256;	Indels 135;	Gaps 38;
OY	4 MSPYQNKNEYEILES--SSNNTNTNRYPPAN--NRDMSTMWNCQGIS-----W 50			
Db	1 MSP-NNQNEYIIDATPSTVSNSDNRYPFANEPTNALQNMDYKDYLKMSAGNASEYPGS 59			
OY	51 DEIMESVETITSIGNLIEFVIE----PSLGGINTLLS-IIGKLIPTNRQTVSALSICDL 105			
Db	60 PEVLVSGQDAKAAIDIVGKLLSGVGVPVGLVSLYLTQIIDILWPSEKSGQWEIFMEQV 119			
OY	106 LSIRKEVADSVLSDAIDFQGLKNRYEYLSYLGAWLKD---GKPLQKTNNSDIGQIV 162			
Db	120 BELINQKTAERYANKALSEGLGNVY-QLYVITALEEENPNGSRALRDVNR----- 172			

Db 650 IEFIPVPTTR---EAKEDLEAAKKAVALFT 677

Search completed: December 15, 2005, 11:24:05  
Job time : 170 secs

REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-701C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1156 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 70:  
US-10-099-285-70

Query Match 20.4%; Score 747; DB 4; Length 1156;  
Best Local Similarity 30.6%; Pred. No. 1.4e-50;  
Matches 230; Conservative 130; Mismatches 249; Indels 142; Gaps 31;  
QY 9 NKNEYEILESSNNTNTPN--RYPPANNRDMSTMWNCQG---ISW-DEIWESVETITS 62  
DB 2 NONKHGIIGASCNCASDDVAKYPLANNPYSSALNLSQNSILNWINIIGDAAKEAVS 61  
QY 63 IGINLIEFVIEPSLGG-INTLLSIIGKLI-PTNRQTVSALSICDLLSIIRKEVADSVLSD 120  
DB 62 IGTIVSLTAPSLTGLISIVYDLIGKVGSGGSGISDLSICDLLSIIDLRSQSVLND 121  
QY 121 AIADPDGKLKNRYEYLYSGAWLKDGKPLQKTNNSDIGQLVYVYFKLSERDFNEIL---- 176  
DB 122 GIADFNGLVLYRN-YLEALDSNKN-----PNSASAEELTRPRIADSEPDRLTRGS 174  
QY 177 ---GGSLSRNNAQVLLPTFAQANVOLLRLRDVQYKAQW-----FPFLSAENVRSELI 228  
DB 175 LTNGLSLARQNAQIILLPSFASAAFFHLLLRDTRYGNWGLYNATPFIYQSKLVELI 234  
QY 229 SPNSGCDFTGDYVERLCKTAETNYCLVYQVGLNOIKOGGTGADTWSKNKFRREMTL 288  
DB 235 E-----LYTDYCVHWYRGFNELRQRTSATAWLEFHRYRREMTL 274  
QY 289 AVLDDIIAIPFYDFEYKPLPHTVELTREIYTDVAGY-----SSGTYSWLR--NWPNTFNGL 342  
DB 275 MVLDIVASFSSLDITNYPIETDFQLSRVIYTDPIGVHRSLSRGESWFSFVNAN--FSDL 333  
QY 343 EANGTRGPGLVTLWSKIGIYNEVSRYPAG-----WVGTREHYEDYTKNGIFQRMSTG 395  
DB 334 E-NAIPNRPSPWFLNNMIISTGSLTLPVSPSTDRAARVYGSRDRISPANSQFTELISQ 392  
QY 396 TSNDLRNIDFQNAVYKITSALIMLVGETTARPEYRVSKADPFRVGGPDLNVDAGNGL 455  
DB 393 HTTATQTLGRN--IFRVDSSQA-CNL-NDTT-----YGVNRAVP-----YHDASEG 435  
QY 456 SRMTIESTFPLVLHNGVRGP-----SHRLSNAACVVYV----- 489  
DB 436 QRSVYEG---YIRTTGIDNPRVQNTVLPGENSDIPTPEDYTHLSTINLTGLRQV 491  
QY 490 ----NSRVNVYGTWHTSLKRENIIEANQITQIPAVKSYLYQLNLANAYTVYIKGTHTGD 545  
DB 492 ASNRSSLVYMGWTHKSLARNNTINPDRIITQIPLTK----VDRGTGVSVDNPDGFIGA 547  
QY 546 LIRFLATKSEYNAVYAGGIRLIINNKTAGOSYRIRFRYAADKAAPFSVYLYPGGWSNR 605  
DB 548 LQ-----RTDHGSL-----GVLRVQFPFLHRLRQYRIRVYASTNTRLVS-----NGS 591  
QY 606 FVLSLEKSYSGNY---DDLKYSDFKFAEIIITPPLP--SSNIQMDVEMQANSFQSDVNVVLDK 661  
DB 592 FGTISQNLSTWRLGEDLRYGSAFAREFNTSIRPTASPDQIRLTIEPSFIQREVYV--DR 649  
QY 662 IEFPLPNTTTLEYEGERDLEKTKNAVNDLFT 692  
DB 650 IEFIPVNPTR---EAKEDLEAAKAVASLFT 677

US-11-018-615-12  
Sequence 12, Application US/11018615  
Publication No. US20050138685A1  
GENERAL INFORMATION:  
APPLICANT: Ronald D. Flannagan  
APPLICANT: Andre R. Abad  
TITLE OF INVENTION: Bacillus Cry9 Family Members  
FILE REFERENCE: 035718/285985  
CURRENT APPLICATION NUMBER: US/11/018,615  
CURRENT FILING DATE: 2004-12-21  
PRIOR APPLICATION NUMBER: 60/531,807  
PRIOR FILING DATE: 2003-12-22  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 1156  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis galleriae  
US-11-018-615-12

Query Match 20.4%; Score 747; DB 6; Length 1156;  
Best Local Similarity 30.6%; Pred. No. 1.4e-50;  
Matches 230; Conservative 130; Mismatches 249; Indels 142; Gaps 31;  
QY 9 NKNEYEILESSNNTNTPN--RYPPANNRDMSTMWNCQG---ISW-DEIWESVETITS 62  
DB 2 NONKHGIIGASCNCASDDVAKYPLANNPYSSALNLSQNSILNWINIIGDAAKEAVS 61  
QY 63 IGINLIEFVIEPSLGG-INTLLSIIGKLI-PTNRQTVSALSICDLLSIIRKEVADSVLSD 120  
DB 62 IGTIVSLTAPSLTGLISIVYDLIGKVGSGGSGISDLSICDLLSIIDLRSQSVLND 121  
QY 121 AIADPDGKLKNRYEYLYSGAWLKDGKPLQKTNNSDIGQLVYVYFKLSERDFNEIL---- 176  
DB 122 GIADFNGLVLYRN-YLEALDSNKN-----PNSASAEELTRPRIADSEPDRLTRGS 174  
QY 177 ---GGSLSRNNAQVLLPTFAQANVOLLRLRDVQYKAQW-----FPFLSAENVRSELI 228  
DB 175 LTNGLSLARQNAQIILLPSFASAAFFHLLLRDTRYGNWGLYNATPFIYQSKLVELI 234  
QY 229 SPNSGCDFTGDYVERLCKTAETNYCLVYQVGLNOIKOGGTGADTWSKNKFRREMTL 288  
DB 235 E-----LYTDYCVHWYRGFNELRQRTSATAWLEFHRYRREMTL 274  
QY 289 AVLDDIIAIPFYDFEYKPLPHTVELTREIYTDVAGY-----SSGTYSWLR--NWPNTFNGL 342  
DB 275 MVLDIVASFSSLDITNYPIETDFQLSRVIYTDPIGVHRSLSRGESWFSFVNAN--FSDL 333  
QY 343 EANGTRGPGLVTLWSKIGIYNEVSRYPAG-----WVGTREHYEDYTKNGIFQRMSTG 395  
DB 334 E-NAIPNRPSPWFLNNMIISTGSLTLPVSPSTDRAARVYGSRDRISPANSQFTELISQ 392  
QY 396 TSNDLRNIDFQNAVYKITSALIMLVGETTARPEYRVSKADPFRVGGPDLNVDAGNGL 455  
DB 393 HTTATQTLGRN--IFRVDSSQA-CNL-NDTT-----YGVNRAVP-----YHDASEG 435  
QY 456 SRMTIESTFPLVLHNGVRGP-----SHRLSNAACVVYV----- 489  
DB 436 QRSVYEG---YIRTTGIDNPRVQNTVLPGENSDIPTPEDYTHLSTINLTGLRQV 491  
QY 490 ----NSRVNVYGTWHTSLKRENIIEANQITQIPAVKSYLYQLNLANAYTVYIKGTHTGD 545  
DB 492 ASNRSSLVYMGWTHKSLARNNTINPDRIITQIPLTK----VDRGTGVSVDNPDGFIGA 547  
QY 546 LIRFLATKSEYNAVYAGGIRLIINNKTAGOSYRIRFRYAADKAAPFSVYLYPGGWSNR 605  
DB 548 LQ-----RTDHGSL-----GVLRVQFPFLHRLRQYRIRVYASTNTRLVS-----NGS 591  
QY 606 FVLSLEKSYSGNY---DDLKYSDFKFAEIIITPPLP--SSNIQMDVEMQANSFQSDVNVVLDK 661  
DB 592 FGTISQNLSTWRLGEDLRYGSAFAREFNTSIRPTASPDQIRLTIEPSFIQREVYV--DR 649  
QY 662 IEFPLPNTTTLEYEGERDLEKTKNAVNDLFT 692

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QY 347 TRGPGVTLWLSKIGLYNEVSYB-----FAGVGTGRHYEDYT-KGNGIFORMSGTT- 396
Db 329 TDPSLVLWLGDMTITYGADSYRTPSGDRIGVWYGNINAFYHTGRTDVVNFRTGDTA 388
QY 397 -----SNDLRNIDFONADYK--ITSILAINLVG--ETTARPEYRVSKADFRVVGPDNLN 448
Db 389 YEDPSTFISNILD--DIYKLDLRAAVSTIOGMDTT-----FGVSSRRFPDIRGNQLY 442
QY 449 DAGNGLSRMTTESTFPLVLHNG--VRGFSHRL-----SNAACVYVGNRNVVYGWTH 500
Db 443 QS-NKPYSPSLPTITTFPGESSEGNANDYSHLLCDVKILQEDSSNICRGSLLSHAWTH 501
QY 501 TSLKRENIIEANQITQIPAVKSYLYLONLANAYTVIKGT-HTGGLIRFLRTKSEYNV 559
Db 502 ASLDRNTLPEITQIPAVTAIEUR-----GNSVWAGPGSTGGDLV-----RMSYHSV 551
QY 560 YAGGIRLIINNKTAGOSYRIRFRYAADKAAPF-----SVLYPGMGSGNRFVLSKSY 613
Db 552 WS--FKVYCSEL---KNYVRIRYASHGNCQFLMKRWPSTGVAPQWARRH---NVQCTF 602
QY 614 SGNYDDLKYSDFKFAEITTPPSSNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTLE 673
Db 603 S---NSMRYEAPKYLDITFITPEENNFAFTIDLESQG-----DLFIDKIEIPVSGSAFE 654
QY 674 YEGERDLEKTKAVNDLFTN 693
Db 655 YEGKONIEKTKAVNDLFTN 674

RESULT 13
US-11-018-615-13
; Sequence 13, Application US/11018615
; Publication No. US20050138685A1
; GENERAL INFORMATION:
; APPLICANT: Ronald D. Flannagan
; TITLE OF INVENTION: Bacillus Cry9 Family Members
; FILE REFERENCE: 035718/285985
; CURRENT APPLICATION NUMBER: US/11/018,615
; PRIOR FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: 60/531,807
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1151
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis DSIR517
US-11-018-615-13

Query Match 20.4%; Score 747; DB 6; Length 1151;
Best Local Similarity 30.6%; Pred. No. 1.4e-50;
Matches 230; Conservative 130; Mismatches 249; Indels 142; Gaps 31;

QY 9 NKNEYEILLESSNNTNTPN--RYPFANNRDMSTMNDCCQ---LSW-DEIWESEVETITS 62
Db 2 NQNKHGIIGASCCGASDDVAKYPLANNPYSSALNLSQNSILNINIIGDAAKEAVS 61
QY 63 IGINLIEFVIEPSLGG-INTLSIIGKLI-PTNRQTVSALSICDLISIRKEVADSVLSD 120
Db 62 ICTIVSLITAPSLTGLISIVYDLIGKVLGGSSGQISDLISICDLISIDLVRVQSGLND 121
QY 121 ATADFDGKLKNRYEYLYSLGAWLKDGPLOKTNNSDITGOLVYFKLSERDFNEIL---- 176
Db 122 GIADFNGLVLYRN-YLEALDSWNKN-----PNSASAEELRTPRIADSEFDRLTRGS 174
QY 177 ---GGSLRNNAQVLLLPFAQAAVQILLERDAVOYKAQW-----FPFLSAENVRSLEI 228
Db 175 LTNGSLAKQNAQIILLPSFASAAFPHLLLLLRDARTYGNWGLYNATPFINYQSKLVELI 234
QY 229 SPNSGCDFTGDYIERLCKTKATYTNVYCYWGLNQIKQGGTGADTWKSKFNKFRREMTL 288

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Db 235 E-----LYTDYCVHWYNRGNELRQGTSAATWLEFHRVREMTL 274
QY 289 AVLDIILAIFFYDEKYPPLPHTBELTREIYDVGY-----SSGTYSMRL--NWPNTFNL 342
Db 275 MVLDIVASFSLDITNPIETDFQLSRVIYTDPIGFWHRSSLRGESWPSFVNRRAN-FSDL 333
QY 343 EANGTRGPGVTLWLSKIGLYNEVSYBAG-----WVGTRHYEDYTKNGIFORMSGT 395
Db 334 E-NAIPNRPSPFWLNNMIISTGSLTPVSPSTDRARVWYGSRRDRISPANSQFTELISQ 392
QY 396 TSNDLRNIDFONADYKITSLAINLVGETTARPEYRVSKADFRVVGPDNLNIDAGNGL 455
Db 393 HTTATQITLGN--IPVDSQA-CNL-NDTT-----YGVNRAVF-----YHDASEGS 435
QY 456 SRMTIESTFPLVLHNSGVGRP-----SHRLSNAACVYVYV----- 489
Db 436 QRSVYEG-----YIRTTGIDNPRVQINITYLPGENSDIPTPEDYTHILSTTNLTGLRQV 491
QY 490 ---NSRVNVYGWTHSLKRENIIEANQITQIPAVKSYLYLONLANAYTVIKGTHHTCGD 545
Db 492 ASNRSSLVWYGTWTHKSLARNNTINPRITQIPLTK-----VDTRGTGVSYVNDPGFIGA 547
QY 546 LIRFLRTKSEYNVYAGGGIRLIINNKTAGOSYRIRFRYAADKAAPFVSVLYPGMGSGNR 605
Db 548 LLQ-----RTDHGSL-----GVLRVQFPLHLRQYRIRVRYASTTNIRLSV-----NGS 591
QY 606 FVSLEKSYSGNY-----DLKYSDFKFAEITTPPLP--SSNIQMDVEMQANSFQSDVNVVLDK 661
Db 592 FGTISQNLPTMRLGEDLRYGSPAIRFNTSIRPTASPDQIRLTIEPSFIRQEVVYV--DR 649
QY 662 IEFLPSNTTILEYGERDLEKTKAVNDLFTN 692
Db 650 IEFIPVNPTR---BAKDELAAKKAVASLFT 677

RESULT 14
US-10-099-285-70
; Sequence 70, Application US/10099285
; Publication No. US20030105319A1
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; Narva, Kenneth E.
; Walz, Michelle
; Stockhoff, Brian
; Muller-Cohn, Judy
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/099,285
; FILING DATE: 15-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/002,285
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.

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Db      552 WS---FKVYCSSEL---KNYVRIRYASHGNCQFLMKRWPSGTGVA PQMARH---NVQGT 602
Qy      614 SGNVDDLYKSDFKFABIITPPLPSSNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTLE 673
Db      603 S---NSMRYEAFKYLDITFTPEENNFAFTIDLESQG---DLFDKIEFIPVSGSAFE 654
Qy      674 YEGERDLEKTKNAVNDLFTN 693
Db      655 YEGKQNIKTQKAVNDLFIN 674

RESULT 11
US-10-783-417-15
; Sequence 15, Application US/10783417
; Publication No. US20040216186A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-006, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274146
; CURRENT APPLICATION NUMBER: US/10783,417
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,806
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 674
; TYPE: PRN
; ORGANISM: Bacillus thuringiensis
US-10-783-417-15

Query Match      22.7%; Score 831; DB 5; Length 674;
Best Local Similarity 31.9%; Pred. No. 1.2e-57;
Matches 236; Conservative 131; Mismatches 257; Indels 116; Gaps 31;

Qy      4 MSPYQNKNEYEILESSNNNTNPNRYPPANN-----RDMSTMSW-NDCOG--ISWDEIWE 55
Db      1 MNQYQNKNEYEILESSQNNMNNPNRYPPADDPNAVMMKNGYKDWNECEGNSISPSAAA 60
Qy      56 SVETITSGINLIEFIEBPSLGGINTLLSIIGKLIPTNRQTVSALSICDLSIIIRKEVAD 115
Db      61 ITSQIVSVILKTLAKAVASSLA--DSIKSSLGISKTITENNVSQVMVQVHQIINRRIOE 118
Qy      116 SVLSDAIADFDGKLKNRYEYLYSYLGAWLKDGKPLQKTNNSDIG---QLVYFVKLSERDF 172
Db      119 TILDGESSLGLVAIYNRDYLGALEAW-----NNKNSINQTNVAEAFKTVVEREF 170
Qy      173 NEILGSSLRNNAQVLLPTFAQANVQLLLRDVQYKAQVFPFLSAENVSELSISPS 232
Db      171 FTKLGIYRTSSQITLLPTTQAAHLMLRDVAVMYQEGW-----NLQSHI----- 218
Qy      233 GCDFTGDIYERLKCKTAETNTYCLWYQVGLNQIKQGGTGADTWGKFNKFRREMTLAVLD 292
Db      219 -----NYSKELDDALEDYTCVEYTKGLNALR--GSTAID-WLEFNSFRDMLTAVLD 270
Qy      293 IIAIPTYDFEYKPLPHTVELTREIYTDVAVGSSGTYSWLRNWPNT-----FNGLEANG 346
Db      271 LVAIFFNPVRYPLSTKISLSRKIYTDVPVGRDTSPS---FGDWTNTGRTLNFANDLEREV 328
Qy      347 TRGPGIATVLSKIGIYNEVVSRY-----FAGVWGTTHYEDYT-KNGNIFQMSGTT- 396
Db      329 TDSPLSVRLWLGDMTITGADISYRTPSPGDRIGVWYGNINAFYHGTGRTDVNMFQGTDTA 388
Qy      397 ----SNDLRNIDFQNAVYK--ITSLAIMNLVG--ETTARPEYRVSKADFRVVGPGDNLN 448
Db      389 YEDPSTFISNILYD--DIYKLDRAAAVSTIQGAMDDT---FGVSSSRFFDIRGNQLY 442
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Qy      449 DAGNNGLSRMTIESTFPPLVLHSGN-VRGPSHRL-----SNAACVYVGNRNVVYGVWTH 500
Db      443 QS-NKPYPSLPITITPPGESSEGNANDYSHLLCDVKILQEDSSNICRGRSSLLSHAWTH 501
Qy      501 TSLKRENIIEANQITQIPAVKSYLQNYLANAVTYVIKGT-HTGGDLIRFLRTKSEYNV 559
Db      502 ASLDRNNTLPEITQIPATAYELR-----GNSSVVAGPGSTGGOLV-----KMSYHSV 551
Qy      560 YAGGGIRLIINNKTAGQSYRIRFRAADKAAPF-----SVLYPGGWSNRNRFVLSKSY 613
Db      552 WS---FKVYCSSEL---KNYVRIRYASHGNCQFLMKRWPSGTGVA PQMARH---NVQGT 602
Qy      614 SGNVDDLYKSDFKFABIITPPLPSSNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTLE 673
Db      603 S---NSMRYEAFKYLDITFTPEENNFAFTIDLESQG---DLFDKIEFIPVSGSAFE 654
Qy      674 YEGERDLEKTKNAVNDLFTN 693
Db      655 YEGKQNIKTQKAVNDLFIN 674

RESULT 12
US-10-781-979-22
; Sequence 22, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10781,979
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 674
; TYPE: PRN
; ORGANISM: Bacillus thuringiensis
US-10-781-979-22

Query Match      22.7%; Score 831; DB 5; Length 674;
Best Local Similarity 31.9%; Pred. No. 1.2e-57;
Matches 236; Conservative 131; Mismatches 257; Indels 116; Gaps 31;

Qy      4 MSPYQNKNEYEILESSNNNTNPNRYPPANN-----RDMSTMSW-NDCOG--ISWDEIWE 55
Db      1 MNQYQNKNEYEILESSQNNMNNPNRYPPADDPNAVMMKNGYKDWNECEGNSISPSAAA 60
Qy      56 SVETITSGINLIEFIEBPSLGGINTLLSIIGKLIPTNRQTVSALSICDLSIIIRKEVAD 115
Db      61 ITSQIVSVILKTLAKAVASSLA--DSIKSSLGISKTITENNVSQVMVQVHQIINRRIOE 118
Qy      116 SVLSDAIADFDGKLKNRYEYLYSYLGAWLKDGKPLQKTNNSDIG---QLVYFVKLSERDF 172
Db      119 TILDGESSLGLVAIYNRDYLGALEAW-----NNKNSINQTNVAEAFKTVVEREF 170
Qy      173 NEILGSSLRNNAQVLLPTFAQANVQLLLRDVQYKAQVFPFLSAENVSELSISPS 232
Db      171 FTKLGIYRTSSQITLLPTTQAAHLMLRDVAVMYQEGW-----NLQSHI----- 218
Qy      233 GCDFTGDIYERLKCKTAETNTYCLWYQVGLNQIKQGGTGADTWGKFNKFRREMTLAVLD 292
Db      219 -----NYSKELDDALEDYTCVEYTKGLNALR--GSTAID-WLEFNSFRDMLTAVLD 270
Qy      293 IIAIPTYDFEYKPLPHTVELTREIYTDVAVGSSGTYSWLRNWPNT-----FNGLEANG 346
Db      271 LVAIFFNPVRYPLSTKISLSRKIYTDVPVGRDTSPS---FGDWTNTGRTLNFANDLEREV 328
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; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274148
; CURRENT APPLICATION NUMBER: US/10/782,096
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,633
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 674
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
US-10-782-096-21

Query Match      22.7%; Score 831; DB 4; Length 674;
Best Local Similarity 31.9%; Pred. No. 1.2e-57;
Matches 236; Conservative 131; Mismatches 257; Indels 116; Gaps 31;

QY      4 MSPYQNKNEYEILESSNNNTNPNRYPPANN-----RDMSTMSW-NDCCG--ISMDEIWE 55
Db      1 MNQYQNKNEYEILESSNNMNPYPFADDPNAVKNKNGYKDWNECEGNSISPSAAA 60

QY      56 SVETITSGINLIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLISIRKEVAD 115
Db      61 ITSXIVSVLKTAKAVASSLA--DSIKSSLGISKTITENNVSQVSMVQVHQIINRRIOE 118

QY      116 SVLSDAIAIDFGKLNKRYEYLSYLGAWLKDGKPLQKTNNSDIG---OLVYFVKLSERDF 172
Db      119 TILDGESSLGLVAIYRDYLGALAW-----NNKSNINQTNVAEAFKTVREF 170

QY      173 NEILGSSLRNNAQVLLPTFAQANVQLLLRDVAVQYKAQFPFLSAENVRSELSISPS 232
Db      171 FTKLGIYRTSSSQITLLPTFTAANLHLSMLRDVAVYQEGW-----NLQSHI----- 218

QY      233 GCDFTGDYERLCKTAETNTYCLYQVGLNQIKQGGTGADTWSKFNKFRREMTLAVLD 292
Db      219 -----NYSKELDDALEDTNYCDEVYTKGLNALR--GSTAID-WLEFNSFRDMLAVLD 270

QY      293 IIAIPFYDFEYKPLPHTVELTREIYTDVAVGSSGTYSWLRNPNT-----FNGLEANG 346
Db      271 LVAIFPNYNPVRYPLSTKISLRKIYTDVGRDTSFS--FGDWTNIGRTLAFNFDLREVE 328

QY      347 TRGPLVTWLSKIGIYNEYVSRV-----FAGVGTGRHYEDYT-KGNGIFQRMSTGTT- 396
Db      329 TDSPLVKWLGDMTIYTGAIIDSYRPTSPGDRIGVWYGNINAFYHTGRTDVVMFRQTGDTA 388

QY      397 -----SNDLNDIFQNAVYK--ITSLAIMNLVG--ETTARPEYRVSKADFRVGGPDJNY 448
Db      389 YEDPSTFISNLYD--DIYKLDLRAAAVSTIQAMDIT---FGVSSSRFFDIRGNOLY 442

QY      449 DAGNGLSRMTTESTFPLVLHNSG--VRGPSHRL-----SNAACVYGNRNVVYGVWTH 500
Db      443 QS-NKPYPSLPITITFPGESSEGNANDYSHLLCDVKILOEDSSNICGRSLLSHAWTH 501

QY      501 TSLKRENIIEANQITQIPAVKSYIQLNYLANAYTVYIKGT-HTGGDLIRFLRTKSEYNV 559
Db      502 ASLDRNNTILPEITQIPAVTAYELR-----GNSSVWAGPGSTGGDLV-----KMSYHSV 551

QY      560 YAGGIRLIINNKTAGOSYRIRFRYAADKAFF-----SVLYPGGWSGNRFRVLSKSY 613
Db      552 WS---FKVYCSL---KNYRVIRYASHGNCQFLMKRVPSTGVAPROWARH---NVQGTG 602

QY      614 SGNYDDLYKDFKFAEITIPPLSSNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTLE 673
Db      603 S---NSMYEAKYIDIFITTEENNFAFTIDLESGL-----DLFIDKIEFIPVSGSAFE 654

QY      674 YEGERDLEKTKNAVNDLFTN 693
      |||:||||:||||:||||:

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Db      655 YEGKQNIETKQKAVNDLFIN 674

RESULT 10
US-10-782-570-17
; Sequence 17, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 674
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
US-10-782-570-17

Query Match      22.7%; Score 831; DB 4; Length 674;
Best Local Similarity 31.9%; Pred. No. 1.2e-57;
Matches 236; Conservative 131; Mismatches 257; Indels 116; Gaps 31;

QY      4 MSPYQNKNEYEILESSNNNTNPNRYPPANN-----RDMSTMSW-NDCCG--ISMDEIWE 55
Db      1 MNQYQNKNEYEILESSNNMNPYPFADDPNAVKNKNGYKDWNECEGNSISPSAAA 60

QY      56 SVETITSGINLIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLISIRKEVAD 115
Db      61 ITSXIVSVLKTAKAVASSLA--DSIKSSLGISKTITENNVSQVSMVQVHQIINRRIOE 118

QY      116 SVLSDAIAIDFGKLNKRYEYLSYLGAWLKDGKPLQKTNNSDIG---OLVYFVKLSERDF 172
Db      119 TILDGESSLGLVAIYRDYLGALAW-----NNKSNINQTNVAEAFKTVREF 170

QY      173 NEILGSSLRNNAQVLLPTFAQANVQLLLRDVAVQYKAQFPFLSAENVRSELSISPS 232
Db      171 FTKLGIYRTSSSQITLLPTFTAANLHLSMLRDVAVYQEGW-----NLQSHI----- 218

QY      233 GCDFTGDYERLCKTAETNTYCLYQVGLNQIKQGGTGADTWSKFNKFRREMTLAVLD 292
Db      219 -----NYSKELDDALEDTNYCDEVYTKGLNALR--GSTAID-WLEFNSFRDMLAVLD 270

QY      293 IIAIPFYDFEYKPLPHTVELTREIYTDVAVGSSGTYSWLRNPNT-----FNGLEANG 346
Db      271 LVAIFPNYNPVRYPLSTKISLRKIYTDVGRDTSFS--FGDWTNIGRTLAFNFDLREVE 328

QY      347 TRGPLVTWLSKIGIYNEYVSRV-----FAGVGTGRHYEDYT-KGNGIFQRMSTGTT- 396
Db      329 TDSPLVKWLGDMTIYTGAIIDSYRPTSPGDRIGVWYGNINAFYHTGRTDVVMFRQTGDTA 388

QY      397 -----SNDLNDIFQNAVYK--ITSLAIMNLVG--ETTARPEYRVSKADFRVGGPDJNY 448
Db      389 YEDPSTFISNLYD--DIYKLDLRAAAVSTIQAMDIT---FGVSSSRFFDIRGNOLY 442

QY      449 DAGNGLSRMTTESTFPLVLHNSG--VRGPSHRL-----SNAACVYGNRNVVYGVWTH 500
Db      443 QS-NKPYPSLPITITFPGESSEGNANDYSHLLCDVKILOEDSSNICGRSLLSHAWTH 501

QY      501 TSLKRENIIEANQITQIPAVKSYIQLNYLANAYTVYIKGT-HTGGDLIRFLRTKSEYNV 559
Db      502 ASLDRNNTILPEITQIPAVTAYELR-----GNSSVWAGPGSTGGDLV-----KMSYHSV 551

QY      560 YAGGIRLIINNKTAGOSYRIRFRYAADKAFF-----SVLYPGGWSGNRFRVLSKSY 613

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; LENGTH: 669
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-5

Query Match      42.7%; Score 1561.5; DB 4; Length 669;
Best Local Similarity 47.1%; Pred. No. 2.3e-116;
Matches 338; Conservative 107; Mismatches 197; Indels 75; Gaps 18;

QY 4 MSPYQKNYEILESSNNNTNTPNRYPPANNRDMSTMSWNDCCOGISWDEIWESEVETITS 63
Db 1 MNSYQNTNEYILDSPNNTMSNRYPPAFKDPNIPINLDACGRPWQDTWESVDIVTI 60
QY 64 GINLIEPIEPSGGINTLLSIIGKLPNTNRTQVTSALSIDLSSIIRKEVADSVLSDATA 123
Db 61 GTYLQELLEPGGIPGIVPISINKLIPSSGQVAALSICDLVSIIRKEVDESVDGVA 120
QY 124 DFDGKLNRYEYLSYLGAWLKDGKPLQKTNNSDIGOLVYVFKLSERDFNEILGGSLSRN 183
Db 121 DFGEMTAYODYLHYLEDWLT-----KSNPKKLADVVKQFOAREDFTKLAGLSRQ 175
QY 184 NAQVLLPTPAQAANVOLLRLRDVAVYKAQWFFLSAENVRSLSISPNSGCDFTGDYIER 243
Db 176 KABILLPTVQAANVHLLRLRDVAVYKKEW-----GLVCPPLYPGSG---RTDCNER 225
QY 244 LKCKTAETNYCLVYQVGLNOIKOGTGADTWSKKNKFRREMTLAVLDIIAIFPYDPE 303
Db 226 LKAKIKETNYCVGWYKGLDQIRQAGTSAEVNKKFNKFRREMTLAVLDIIAIFPYDPE 285
QY 304 KYPLTHVELTRIYTDVAVYSGTYSWLRNWNPTFNGLEANGTRGPGVLTWLSKGIYN 363
Db 286 KYPLATSVELTRIYTDVAVYSGTYSGNNGWERFP--SFNSVEANGTRGPGVLTWLSK 343
QY 364 EYVS---RYPAGVWGRHYEDYTKNGI FORMSGTTSNDLRNIDFQNAVYKITSL---A 417
Db 344 HSINLQGLSGWGGTRHYEDFTKNGAFORMSGTTSNNPRNIFGNTDIFKIISLARYA 403
QY 418 INNLVGETTARPEYRVSKADPRVCGPDLYDAGNGLSMTIESTFPLVLSNGVR---474
Db 404 MQPFVGYSI--PRLVSRAEFFPTTLNTFLYEVNSGYSQ-TIESVLP-----GINKDL 454
QY 475 -----GFSHRLSNAACVYVNSRVVYVWTHTSKRENIIEANQITQIPAVKSYLQNYL 529
Db 455 PPSRTNYSHRLSNAACVQNETSRVNVFGWTHTSKDKNRIYDPKIQITQIPAVKAFALPAGT 514
QY 530 ANAYTVIKGT-HTGDLIRFLRTKSEYNNAVAGGIRLIINNKTAGQSYRIRFRYAADK 588
Db 515 GVAGGYVTAGPGVTGGDVTL-----PYQA-----SLKIRLTSAPTKNRYRRLRYASGG 564
QY 589 AAFPSVLYPGGWSNRFVSLEKSYSGNYDDLKYSDPKFAEITPPLPSNTQMOMVEMQA 648
Db 565 PGFPRVERSPSSVSN--ANFSRPATGG-----YSSFYVDVTLVTTFNOSGVEIIQN-- 615
QY 649 NSPQSDVNVLDKIEFLP-----SNTTILEYEG-----RDLEKTKNAVNDLFTN 693
Db 616 ---LSGHLIVDKVEFIPIDIQIEKTKCFQEGDICRCBGVQSLETKKIVNSLFIN 669
```

## RESULT 8

```
US-10-782-141-20
; Sequence 20, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10782,141
; CURRENT FILING DATE: 2004-02-20
```

```
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-20
```

```
Query Match      22.7%; Score 831; DB 4; Length 674;
Best Local Similarity 31.9%; Pred. No. 1.2e-57;
Matches 236; Conservative 131; Mismatches 257; Indels 116; Gaps 31;

QY 4 MSPYQKNYEILESSNNNTNTPNRYPPANNRDMSTMSW-NDCCG--TSWDEIWE 55
Db 1 MNQYQKNYEILESSQNNMNPYFPADDPNAVKNKYKDWVNECEGSNPSAAA 60
QY 56 SVETITSIGINLIEPIEPSLGGINTLLSIIGKLPNTNRTQVTSALSIDLSSIIRKEVAD 115
Db 61 ITSIVSIVLTKLAKAVASSLA--DSIKSSLGISKTITENNVSQVSMVQVHQIINRIQE 118
QY 116 SVLSDAIADFDGKLNRYEYLSYLGAWLKDGKPLQKTNNSDIG---QLVYVFKLSERDF 172
Db 119 TILDGESSLNGLVAIYNRDYLGALAW-----NNKSNINYQTNVAEAKTVEREF 170
QY 173 NEILGGSLSRNAQVLLPTPAQAANVOLLRLRDVAVYKAQWFFLSAENVRSLSISPN 232
Db 171 FTKLAGIVRTSSQITLPTFTQAANLHLSMLRDVAVYQEGM-----NLQSHI----- 218
QY 233 GCDFTGDYIERLKCKTAETNYCLVYQVGLNOIKOGTGADTWSKKNKFRREMTLAVLD 292
Db 219 -----NYSKELDDALEDYTCVEYTKGLNALR-GSTAID-WLEFNSFRDMLTMLVD 270
QY 293 IIAIPTVDPEKYPVTHVELTRIYTDVAVYSGTYSWLRNWNPT-----FNGLEANG 346
Db 271 LVAIPTNPNVRYPLSTKISLSRKIYTDVPGRTDPS--FGDWTNTRTLANPNDLREVR 328
QY 347 TRGPGVLTWLSKIGIYNEVYSY-----PAGWVGRHYEDYT-KNGIIFORMSGTT- 396
Db 329 TDSPLVKWLGDMTIVTGAIDSYRPTSPGDRIGVWYGNINAFVHTGRTDVMFRQTGDTA 388
QY 397 -----SNDLRNIDFQNAVYK--ITSIAIMNLVG--ETTARPEYRVSKADPRVCGPDLY 448
Db 389 YEDPFTFISNILD--DIYKLDLRAAAVSTIQGAMDIT---FGVSSSRFFDIRGNQLY 442
QY 449 DAGNGLSRMTTESTFPLVLSNG-VRGPSHRL-----SNAACVYVNSRVVYVWTH 500
Db 443 QS-NKPYPSLPITITFPGEESEGNANDYSHLLCDVKILOEDSSNICGRSSLLSHAWTH 501
QY 501 TSLKRENIIEANQITQIPAVKSYLQNYLANAYTVIKGT-HTGDLIRFLRTKSEYNNAV 559
Db 502 ASLDRNNTILPDEITQIPAVTAYELR-----GNSSVWAGPGSTGGDLV-----KMSYHSV 551
QY 560 YAGGIRLIINNKTAGQSYRIRFRYAADKAAFP-----SVLYPGGWSNRFVSLEKSY 613
Db 552 WS---FKVYCSL---KNYVRIRYASHGNCQFLMKRWPFSTGVAPQWRAH---NVQGTFF 602
QY 614 SGNVDDLKYSDFKFAEITPPLPSNINQMDVEMQANSFQSDVNVLDKIEFLPSNTTILE 673
Db 603 S---NSMYEAPKYLDIITIPENNPAFTIDLESQG-----DLFIDKIEFIPVSGSAFE 654
QY 674 YEGERDLEKTKNAVNDLFTN 693
Db 655 YEGKQIEKTKNAVNDLFIN 674
```

## RESULT 9

```
US-10-782-096-21
; Sequence 21, Application US/10782096
; Publication No. US20040210964A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
```

Db 3 YENKNEYELLESSNNTPNPNRYPPANNRDMSTMSNDCCQGISWDEIWESAEITISIGD 62  
Qy 67 LIEFVIEPSLGINTLLSIIGKLIPTNQTVSALSICDLSIIIRKEVADSVLSDAIADP- 125  
Db 63 LIEFLMEPSLGINTLLSIIGKLIPTNHOSVBSALSICDLSIIIRKEVADSVLSDAICRFL 122  
Qy 126 DCKLKNRYEYLYSGAWLKDGKPLQKTNNSDYGOLVYFKLSERDFEILGGSISRNNA 185  
Db 123 DCKLKNRYEYLYPYLEAMUKDGKPLQKTNNSDYGOLVYFKLSERDFEILGGSISRNNA 182  
Qy 186 QVLLPTFAQAANVQLLLRDADVOYKAQWFFPFLSAENVRSELISPNSGCDFTGDIYERLK 245  
Db 183 QIILLPYFCASCCKQLLLRDADVOYEQWFFPFLSAENVRSELISPNSGCDFTGDIYERLK 242  
Qy 246 CKTAETNTYCLVYQVGLNQIKQGGTADTWKFNKFRREMTLAVLDIIAIPPTVDFEY 305  
Db 243 CKIAEYTDYCEYQVGLNQIKQGGTADTWKFNKFRREMTLAVLDIIAIPPTVDFEY 302  
Qy 306 PLPTHVELTREIYTDVAGVSSGTYSWLRNWPNTFNGLEANGTRGPGVLTWLSKIGYNEY 365  
Db 303 PLPTHVELTREIYTDVAGVSSGTYSWLRNWPNTFNGLEANGTRGPGVLTWLSKIGYNEY 362  
Qy 366 VSRYPAGWGTREIYTDVAGVSSGTYSWLRNWPNTFNGLEANGTRGPGVLTWLSKIGYNEY 425  
Db 363 VSRYPAGWGTREIYTDVAGVSSGTYSWLRNWPNTFNGLEANGTRGPGVLTWLSKIGYNEY 422  
Qy 426 TARPEYRVSKADPRRGGPDLNDYDAGNGLSRMTIESTFPPLVHNSGVGRP- 478  
Db 423 NARPEYRVSKADPRRGGPDLNDYDAGNGLSRMTIESTFPPLVHNSGVGRP- 476  
Qy 479 RLSNAAACVVGNSRVNVGTHWTHSLKRENIIEANOITQIPAVKSVYLYQLNLANAYTVIK 538  
Db 477 RLSNAAACVVGNSRVNVGTHWTHSLKRENIIEANOITQIPAVKSVYLYQLNLANAYTVIK 533  
Qy 539 GT-HTGGDLIRFLRTKSEYNAVYAGGIRLIINNKTAGOSYRIRPRYAADKAAFPSPVLY 597  
Db 534 GPHTGGNVVSL- 579  
Qy 598 PCGWSNRFVLSLEKY- 652  
Db 580 VERWSFS- 627  
Qy 653 SDNVVLDKIEFLPNTTLEVEGERDLEKTKNAVNDLF 691  
Db 628 TFINV- 664

RESULT 6  
US-10-782-141-3  
; Sequence 3, Application US/10782141  
; Publication No. US20040197917A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274143  
; CURRENT APPLICATION NUMBER: US/10/782,141  
; PRIOR FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: 60/448,632  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 672  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-141-3

Query Match 43.0%; Score 1571.5; DB 4; Length 672;  
Best Local Similarity 47.2%; Pred. No. 3.6e-117;  
Matches 340; Conservative 107; Mismatches 196; Indels 75; Gaps 18;  
Qy 1 MKKNSPYQNKNEYELLESSNNTPNPNRYPPANNRDMSTMSNDCCQGISWDEIWESVETI 60  
Db 1 MKKNSPYQNKNEYELLESSNNTPNPNRYPPANNRDMSTMSNDCCQGISWDEIWESVETI 60  
Qy 61 TSIGINLIEFVIEPSLGINTLLSIIGKLIPTNQTVSALSICDLSIIIRKEVADSVLS 120  
Db 61 TSIGINLIEFVIEPSLGINTLLSIIGKLIPTNQTVSALSICDLSIIIRKEVADSVLS 120  
Qy 121 AIADPDGKLNRYEYLYSGAWLKDGKPLQKTNNSDYGOLVYFKLSERDFEILGGSIS 180  
Db 121 AIADPDGKLNRYEYLYSGAWLKDGKPLQKTNNSDYGOLVYFKLSERDFEILGGSIS 180  
Qy 121 GVADPEGEMTAQDIYLYHLEDWLT- 175  
Db 121 GVADPEGEMTAQDIYLYHLEDWLT- 175  
Qy 181 SRNNAQVLLPTFAQAANVQLLLRDADVOYKAQWFFPFLSAENVRSELISPNSGCDFTGDIY 240  
Db 181 SRNNAQVLLPTFAQAANVQLLLRDADVOYKAQWFFPFLSAENVRSELISPNSGCDFTGDIY 240  
Qy 176 SRQKAEIILLPTFYQAANVHLLLRDADVKYKKEW- 225  
Db 176 SRQKAEIILLPTFYQAANVHLLLRDADVKYKKEW- 225  
Qy 241 YERLKCKTAETNTYCLVYQVGLNQIKQGGTADTWKFNKFRREMTLAVLDIIAIPPTY 300  
Db 241 YERLKCKTAETNTYCLVYQVGLNQIKQGGTADTWKFNKFRREMTLAVLDIIAIPPTY 300  
Qy 226 NERLKAIKETNTYCVGWYKNGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIPPTY 285  
Db 226 NERLKAIKETNTYCVGWYKNGLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIPPTY 285  
Qy 301 DPEKYPLPTHVELTREIYTDVAGVSSGTYSWLRNWPNTFNGLEANGTRGPGVLTWLSKIG 360  
Db 301 DPEKYPLPTHVELTREIYTDVAGVSSGTYSWLRNWPNTFNGLEANGTRGPGVLTWLSKIG 360  
Qy 286 DPEKYPLATHVELTREIYTDVAGVSSGTYSWLRNWPNTFNGLEANGTRGPGVLTWLSKIG 343  
Db 286 DPEKYPLATHVELTREIYTDVAGVSSGTYSWLRNWPNTFNGLEANGTRGPGVLTWLSKIG 343  
Qy 361 IYNEBVS- 416  
Db 361 IYNEBVS- 416  
Qy 344 IYSHINLQCYLSCWGGTTHYEDYTKGNGAFQMSGTTNNPRNIIFGNTDIPKIIISLA 403  
Db 344 IYSHINLQCYLSCWGGTTHYEDYTKGNGAFQMSGTTNNPRNIIFGNTDIPKIIISLA 403  
Qy 417 --AIMNLVGETTARPEYRVSKADPRRGGPDLNDYDAGNGLSRMTIESTFPPLVHNSGV 474  
Db 417 --AIMNLVGETTARPEYRVSKADPRRGGPDLNDYDAGNGLSRMTIESTFPPLVHNSGV 474  
Qy 404 RYANQPPFVYGI- 454  
Db 404 RYANQPPFVYGI- 454  
Qy 475 -----GPSHRLSNAACVVGNSRVNVGTHWTHSLKRENIIEANOITQIPAVKSVYLYQ 526  
Db 475 -----GPSHRLSNAACVVGNSRVNVGTHWTHSLKRENIIEANOITQIPAVKSVYLYQ 526  
Qy 455 KDLPPSRNTYSHRLSNAACVQNETSRNVGTHWTHSLKRENIIEANOITQIPAVKSVYLYQ 514  
Db 455 KDLPPSRNTYSHRLSNAACVQNETSRNVGTHWTHSLKRENIIEANOITQIPAVKSVYLYQ 514  
Qy 527 NYLANAYTVIKGT-HTGGDLIRFLRTKSEYNAVYAGGIRLIINNKTAGOSYRIRPRY 585  
Db 527 NYLANAYTVIKGT-HTGGDLIRFLRTKSEYNAVYAGGIRLIINNKTAGOSYRIRPRY 585  
Qy 515 AGTGAGVYTAGPGYTGDDVVT- 564  
Db 515 AGTGAGVYTAGPGYTGDDVVT- 564  
Qy 586 ADKAAFPSPVLYPCGWSNRFVLSLEKSYSGNYDDLKYSDFKFAEITPPLSSNIQMDVE 645  
Db 586 ADKAAFPSPVLYPCGWSNRFVLSLEKSYSGNYDDLKYSDFKFAEITPPLSSNIQMDVE 645  
Qy 565 SGGPFPFRVERWSPSSVSN- 617  
Db 565 SGGPFPFRVERWSPSSVSN- 617  
Qy 646 MQANSFQSDNVNVLDKIEFLP- 693  
Db 646 MQANSFQSDNVNVLDKIEFLP- 693  
Qy 618 N-----LSGYHLIVDKVEFIPIDIQIEKCTKQCEGDCIRCEGVQSLETKKEIVNSLFIN 672  
Db 618 N-----LSGYHLIVDKVEFIPIDIQIEKCTKQCEGDCIRCEGVQSLETKKEIVNSLFIN 672

RESULT 7  
US-10-782-141-5  
; Sequence 5, Application US/10782141  
; Publication No. US20040197917A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274143  
; CURRENT APPLICATION NUMBER: US/10/782,141  
; PRIOR FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: 60/448,632  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5

```

QY 186 QVLLPTFAAANVQLLLRDADVQYKAQWFPFELSAENVRSSELSPNSGCDFTGDYVERLK 245
:|||||:
DB 183 QI LLLPFCASCCKQLLLRDADVQYEQWFPFELSAENVRSSELSPNSGCDFTGDYVERLK 242
:|||||:
QY 246 CKTAETNYCLYWQVGLNQIKQGGTGADTWKFNKFRREMTLAVLDIITAIPTDYDEKY 305
:|||||:
DB 243 CKIAETDYCEYWQAGLNQIKQAGTGADTWKFNKFRREMTLTVLDIITAIPTDYDEKY 302
:|||||:
QY 306 PLPTHVELTREIYTDVAGYSSGTYSLRNWPNFTNGLEANGTRGPGGLVTLWLSKIGIYNEY 365
:|||||:
DB 303 PLPTHVELTREIYTDVPGYSSGTYSLWKYWTGAFNTLEANGTRGPGGLVTLWLSIGIYNEY 362
:|||||:
QY 366 VSRYPAGWGTREHYEDYTKNGIFQMSGTTNDLNRIDFQNAVYKIITSLAIMLVGET 425
:|||||:
DB 363 VSRYPAGWGTREHYEDYTKNGIFQMSGTTNDLNRIDFQNAVYKIITSLAIMLVGET 422
:|||||:
QY 426 TARPEYRVSKADPRRVGGPDLNVDAGNGLSRMTIESTPPLVLSHNGVRGP-----SH 478
:|||||:
DB 423 NARPEYRVSPAESSESTAFIYLDAGNSGLSMTITSKLP-----GKNPEPSYRDYSH 476
:|||||:
QY 479 RLSNAACVVYGNRNVYGTHTSLKRENIIEANQITQIPAVKSYLYQLNYLANAYTYVIK 538
:|||||:
DB 477 RLSNAACVAGNSRINVYGTHTSMKYNLIYPDKITQIPAVKAFDISD---TGPQGVIA 533
:|||||:
QY 539 GT-HTGGDLIRFLRTKSEYNAVYAGGIRLIINNKTAGOSYRIRFPAADKAFFSVLY 597
:|||||:
DB 534 GPGHTGGNVSL-----PYYSRLKIRLI--PASTNKNYLVRVRYTSTS-----NGRLL 579
:|||||:
QY 598 PGWGSNRFVLSKSY-----SGNYDDLKYSDFKFAEITPPLPSSNIQMDVEMOANSFQ 652
:|||||:
DB 580 VERMSPS---SIINSYFFLPSTGPGDSFGYVD-----TLVTFNPGVEIILQNL 627
:|||||:
QY 653 SDNVVLDKIEFLPSNTTLEYEGERDLEKTKNAVNDLF 691
:|||||:
DB 628 TPINV--DKVEFIPVNSTALEYEGKQLEKAQDVVNDLF 664
:|||||:

RESULT 4
US-10-782-096-23
; Sequence 23, Application US/10782096
; Publication No. US20040210964A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and
; FILE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274148
; CURRENT APPLICATION NUMBER: US/10782,096
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,633
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-096-23

Query Match 63.7%; Score 2329.5; DB 4; Length 666;
Best Local Similarity 67.2%; Pred. No. 4.5e-178;
Matches 470; Conservative 62; Mismatches 116; Indels 51; Gaps 12;

```

```

QY 7 YQNKNEYELLESSNNNTNPNRYPPANNRDMSTMSWDCQGISWDEIWEIVETIISGIN 66
:|||||:
DB 3 YQNKNEYELLESSNNNTNPNRYPPANNRDMSTMSWDCQGISWDEIWEIVETIISGIN 62
:|||||:
QY 67 LIEFVIEPSLGGINTLFSIIIGKLIPTNRQTVSALSICDLLSIIRKEVADSVLSDAICRFL 125
:|||||:

```

```

DB 63 LIEFMEPSLGGINTLFSIIIGKLIPTNHQSVSALSICDLLSIIRKEVADSVLSDAICRFL 122
:|||||:
QY 126 DGKLNRYRYIISYLGAWLKDQKPLQKTNNSDITGLVYFYFKLSERDPNEILGSLSRNNA 185
:|||||:
DB 123 DGKLNRYRYIISYLGAWLKDQKPLQKTNNSDITGLVYFYFKLSERDPNEILGSLSRNNA 182
:|||||:
QY 186 OVLLPTFAAANVQLLLRDADVQYKAQWFPFELSAENVRSSELSPNSGCDFTGDYVERLK 245
:|||||:
DB 183 QI LLLPFCASCCKQLLLRDADVQYEQWFPFELSAENVRSSELSPNSGCDFTGDYVERLK 242
:|||||:
QY 246 CKTAETNYCLYWQVGLNQIKQGGTGADTWKFNKFRREMTLAVLDIITAIPTDYDEKY 305
:|||||:
DB 243 CKIAETDYCEYWQAGLNQIKQAGTGADTWKFNKFRREMTLTVLDIITAIPTDYDEKY 302
:|||||:
QY 306 PLPTHVELTREIYTDVAGYSSGTYSLRNWPNFTNGLEANGTRGPGGLVTLWLSKIGIYNEY 365
:|||||:
DB 303 PLPTHVELTREIYTDVPGYSSGTYSLWKYWTGAFNTLEANGTRGPGGLVTLWLSIGIYNEY 362
:|||||:
QY 366 VSRYPAGWGTREHYEDYTKNGIFQMSGTTNDLNRIDFQNAVYKIITSLAIMLVGET 425
:|||||:
DB 363 VSRYPAGWGTREHYEDYTKNGIFQMSGTTNDLNRIDFQNAVYKIITSLAIMLVGET 422
:|||||:
QY 426 TARPEYRVSKADPRRVGGPDLNVDAGNGLSRMTIESTPPLVLSHNGVRGP-----SH 478
:|||||:
DB 423 NARPEYRVSPAESSESTAFIYLDAGNSGLSMTITSKLP-----GKNPEPSYRDYSH 476
:|||||:
QY 479 RLSNAACVVYGNRNVYGTHTSLKRENIIEANQITQIPAVKSYLYQLNYLANAYTYVIK 538
:|||||:
DB 477 RLSNAACVAGNSRINVYGTHTSMKYNLIYPDKITQIPAVKAFDISD---TGPQGVIA 533
:|||||:
QY 539 GT-HTGGDLIRFLRTKSEYNAVYAGGIRLIINNKTAGOSYRIRFPAADKAFFSVLY 597
:|||||:
DB 534 GPGHTGGNVSL-----PYYSRLKIRLI--PASTNKNYLVRVRYTSTS-----NGRLL 579
:|||||:
QY 598 PGWGSNRFVLSKSY-----SGNYDDLKYSDFKFAEITPPLPSSNIQMDVEMOANSFQ 652
:|||||:
DB 580 VERMSPS---SIINSYFFLPSTGPGDSFGYVD-----TLVTFNPGVEIILQNL 627
:|||||:
QY 653 SDNVVLDKIEFLPSNTTLEYEGERDLEKTKNAVNDLF 691
:|||||:
DB 628 TPINV--DKVEFIPVNSTALEYEGKQLEKAQDVVNDLF 664
:|||||:

```

```

RESULT 5
US-10-781-979-25
; Sequence 25, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; FILE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10781,979
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-781-979-25

Query Match 63.7%; Score 2329.5; DB 5; Length 666;
Best Local Similarity 67.2%; Pred. No. 4.5e-178;
Matches 470; Conservative 62; Mismatches 116; Indels 51; Gaps 12;

```

```

QY 7 YQNKNEYELLESSNNNTNPNRYPPANNRDMSTMSWDCQGISWDEIWEIVETIISGIN 66
:|||||:

```

Db 301 DFEKYPPLPHVELTREIYTDVAGYSSGYSLRWPNFTFNGLEANGTRGPGVLTWLSKIG 360  
Qy 361 IYNEVSRYPAGVGTGTHYEDYTKNGIFQRMSTGTTSDNLRNIDFQNDADVYKITSLSAIMN 420  
Db 361 IYNEVSRYPAGVGTGTHYEDYTKNGIFQRMSTGTTSDNLRNIDFQNDADVYKITSLSAIMN 420  
Qy 421 LVGETTARPEYRVSKADFRVGGPDLDYDAGNGLSRMTIESTFPLVLHSGVRGSPSHRL 480  
Db 421 LVGETTARPEYRVSKADFRVGGPDLDYDAGNGLSRMTIESTFPLVLHSGVRGSPSHRL 480  
Qy 481 SNAACVYVGNRSRVNYGWTHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVVIKGT 540  
Db 481 SNAACVYVGNRSRVNYGWTHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVVIKGT 540  
Qy 541 HTGGDLIRFLRTKSEYNVAVAGGIRLIINNKTAGQSYRIRFPRYAADKAAFFSVLYPGG 600  
Db 541 HTGGDLIRFLRTKSEYNVAVAGGIRLIINNKTAGQSYRIRFPRYAADKAAFFSVLYPGG 600  
Qy 601 WGSNRFVLSKSYSGNYDDLKYSDFKFAEIIITPPLPSSNIQMDVEMOANSFQSDVNVVLD 660  
Db 601 WGSNRFVLSKSYSGNYDDLKYSDFKFAEIIITPPLPSSNIQMDVEMOANSFQSDVNVVLD 660  
Qy 661 KIEFLPSNTTLEYGGERDLEKTKNAVNDLFTN 693  
Db 661 KIEFLPSNTTLEYGGERDLEKTKNAVNDLFTN 693

## RESULT 2

US-10-781-979-5  
; Sequence 5, Application US/10781979  
; Publication No. US20040250311A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274147  
; CURRENT APPLICATION NUMBER: US/10/781,979  
; PRIOR FILING DATE: 2004-02-20  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq For Windows Version 4.0  
; SEQ ID NO 5  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-781-979-5

Query Match 99.6%; Score 3640; DB 5; Length 690;  
Best Local Similarity 100.0%; Pred. No. 2.3e-283;  
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MSPYQNKNEYEILESSNNNTNPNRYPPANNRDMSTMWDCQGISWDEIWESVETITSI 63  
Db 1 MSPYQNKNEYEILESSNNNTNPNRYPPANNRDMSTMWDCQGISWDEIWESVETITSI 60  
Qy 64 GINLEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLSIIRKEVADSVLSDAIA 123  
Db 61 GINLEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLSIIRKEVADSVLSDAIA 120  
Qy 124 DFDGKLKNRYEYLSYLGAWLKDGKPLQKTNNSDYGQVYFKLSERDFNEILGGSLSRN 183  
Db 121 DFDGKLKNRYEYLSYLGAWLKDGKPLQKTNNSDYGQVYFKLSERDFNEILGGSLSRN 180  
Qy 184 NAOVLLPTFAQANVQLLLRDVQYKAQWPFPLSAENVRSSELISPNSGCDFTGDYDER 243  
Db 181 NAOVLLPTFAQANVQLLLRDVQYKAQWPFPLSAENVRSSELISPNSGCDFTGDYDER 240

Qy 244 LKCKTAETNYCLWYQVGLNQIKOGGTGADTWSKFNKFRREMTLAVLDIIAIPPTDPE 303  
Db 241 LKCKTAETNYCLWYQVGLNQIKOGGTGADTWSKFNKFRREMTLAVLDIIAIPPTDPE 300  
Qy 304 KYPLPTHVELTREIYTDVAGYSSGYSLRWPNFTFNGLEANGTRGPGVLTWLSKIGIYN 363  
Db 301 KYPLPTHVELTREIYTDVAGYSSGYSLRWPNFTFNGLEANGTRGPGVLTWLSKIGIYN 360  
Qy 364 EYVSRYFAGVGTGTHYEDYTKNGIFQRMSTGTTSDNLRNIDFQNDADVYKITSLSAIMN 423  
Db 361 EYVSRYFAGVGTGTHYEDYTKNGIFQRMSTGTTSDNLRNIDFQNDADVYKITSLSAIMN 420  
Qy 424 ETTARPEYRVSKADFRVGGPDLDYDAGNGLSRMTIESTFPLVLHSGVRGSPSHRLSNA 483  
Db 421 ETTARPEYRVSKADFRVGGPDLDYDAGNGLSRMTIESTFPLVLHSGVRGSPSHRLSNA 480  
Qy 484 ACVYVGNRSRVNYGWTHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVVIKGTHTG 543  
Db 481 ACVYVGNRSRVNYGWTHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVVIKGTHTG 540  
Qy 544 GDLIRFLRTKSEYNVAVAGGIRLIINNKTAGQSYRIRFPRYAADKAAFFSVLYPGGWS 603  
Db 541 GDLIRFLRTKSEYNVAVAGGIRLIINNKTAGQSYRIRFPRYAADKAAFFSVLYPGGWS 600  
Qy 604 NRVLSKSYSGNYDDLKYSDFKFAEIIITPPLPSSNIQMDVEMOANSFQSDVNVVLDKIE 663  
Db 601 NRVLSKSYSGNYDDLKYSDFKFAEIIITPPLPSSNIQMDVEMOANSFQSDVNVVLDKIE 660  
Qy 664 FLPSNTTLEYGGERDLEKTKNAVNDLFTN 693  
Db 661 FLPSNTTLEYGGERDLEKTKNAVNDLFTN 690

## RESULT 3

US-10-782-141-23  
; Sequence 23, Application US/10782141  
; Publication No. US20040197917A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274143  
; CURRENT APPLICATION NUMBER: US/10/782,141  
; PRIOR FILING DATE: 2004-02-20  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 666  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-141-23

Query Match 63.7%; Score 2329.5; DB 4; Length 666;  
Best Local Similarity 67.2%; Pred. No. 4.5e-178;  
Matches 470; Conservative 62; Mismatches 116; Indels 51; Gaps 12;

Qy 7 YONKNEVEILESSNNNTNPNRYPPANNRDMSTMWDCQGISWDEIWESVETITSI 66  
Db 3 YENKNEVEILESSNNNTNPNRYPPANNRDMSTMWDCQGISWDEIWESVETITSI 62  
Qy 67 LIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLSIIRKEVADSVLSDAIADP- 125  
Db 63 LIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLSIIRKEVADSVLSDAICRFL 122  
Qy 126 DGKLNRYEYLSYLGAWLKDGKPLQKTNNSDYGQVYFKLSERDFNEILGGSLSRNA 185  
Db 123 DGKLNRYEYLSYLGAWLKDGKPLQKTNNSDYGQVYFKLSERDFNEILGGSLSRNA 182

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2005, 11:15:22 ; Search time 168 Seconds  
(without alignments)  
1723.546 Million cell updates/sec

Title: US-10-781-979-3  
Perfect score: 3655  
Sequence: 1 MKKMSPYQNKNEYEILESS.....YEGERDLEKTKNAVNDLFTN 693

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /cgn2\_6/prodata/1/pubpaa/us07\_PUBCOMB.pap:\*
- 2: /cgn2\_6/prodata/1/pubpaa/us08\_PUBCOMB.pap:\*
- 3: /cgn2\_6/prodata/1/pubpaa/us09\_PUBCOMB.pap:\*
- 4: /cgn2\_6/prodata/1/pubpaa/us10A\_PUBCOMB.pap:\*
- 5: /cgn2\_6/prodata/1/pubpaa/us10B\_PUBCOMB.pap:\*
- 6: /cgn2\_6/prodata/1/pubpaa/us11\_PUBCOMB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3655	100.0	693	5 US-10-781-979-3	Sequence 3, Appli
2	3640	99.6	690	5 US-10-781-979-5	Sequence 5, Appli
3	2329.5	63.7	666	4 US-10-782-141-23	Sequence 23, Appl
4	2329.5	63.7	666	4 US-10-782-096-23	Sequence 23, Appl
5	2329.5	63.7	666	5 US-10-781-979-25	Sequence 25, Appl
6	1571.5	43.0	672	4 US-10-782-141-3	Sequence 3, Appli
7	1561.5	42.7	669	4 US-10-782-141-5	Sequence 5, Appli
8	831	22.7	674	4 US-10-782-141-20	Sequence 20, Appl
9	831	22.7	674	4 US-10-782-096-21	Sequence 21, Appl
10	831	22.7	674	4 US-10-782-570-17	Sequence 17, Appl
11	831	22.7	674	5 US-10-783-417-15	Sequence 15, Appl
12	831	22.7	674	5 US-10-781-979-22	Sequence 15, Appl
13	747	20.4	1151	6 US-11-018-615-13	Sequence 13, Appl
14	747	20.4	1156	4 US-10-099-285-70	Sequence 70, Appl
15	747	20.4	1156	6 US-11-018-615-12	Sequence 12, Appl
16	725	19.8	1167	4 US-10-089-678-1	Sequence 1, Appli
17	724	19.8	659	5 US-10-782-141-22	Sequence 22, Appl
18	724	19.8	659	5 US-10-781-979-24	Sequence 24, Appl
19	713.5	19.5	1206	4 US-10-032-717-2	Sequence 2, Appli
20	713.5	19.5	1206	4 US-10-414-637-2	Sequence 2, Appli
21	713.5	19.5	1206	4 US-10-606-320-2	Sequence 2, Appli
22	713.5	19.5	1206	4 US-10-746-914-2	Sequence 2, Appli
23	712	19.5	802	4 US-10-428-961-30	Sequence 30, Appl
24	707.5	19.4	719	5 US-10-428-961-30	Sequence 30, Appl
25	707.5	19.4	719	5 US-10-926-819-31	Sequence 31, Appl
26	705.5	19.3	1228	5 US-10-926-819-8	Sequence 8, Appli
27	702.5	19.2	1228	4 US-10-809-953-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1  
US-10-781-979-3  
; Sequence 3, Application US/10781979  
; Publication No. US20040250311A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Brian  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and  
; FILE REFERENCE: 045600/274147  
; CURRENT APPLICATION NUMBER: US/10/781,979  
; CURRENT FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: 60/448,797  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 693  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-781-979-3  
  
Query Match 100.0%; Score 3655; DB 5; Length 693;  
Best Local Similarity 100.0%; Pred. No. 1.5e-284;  
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MKKMSPYQNKNEYEILESSNNTPNRYPPANNRDMSTMWDCQGISWDEIWESVETI 60  
Db 1 MKKMSPYQNKNEYEILESSNNTPNRYPPANNRDMSTMWDCQGISWDEIWESVETI 60  
  
QY 61 TSIGINLIEFVIEPSLGGINTLLSIIGKLPTNROTVSALSICDLLSIIRKEVADSVLSD 120  
Db 61 TSIGINLIEFVIEPSLGGINTLLSIIGKLPTNROTVSALSICDLLSIIRKEVADSVLSD 120  
  
QY 121 AIADPDGKLKNRYEYLSYLGAWLKDGKPLQKTNNSDYGQVYKQWPFPLSAENVRSSELISPNSGCDPTGDY 180  
Db 121 AIADPDGKLKNRYEYLSYLGAWLKDGKPLQKTNNSDYGQVYKQWPFPLSAENVRSSELISPNSGCDPTGDY 180  
  
QY 181 SRNNAQVLLPTFAQANVQLLLRLDQVYKQWPFPLSAENVRSSELISPNSGCDPTGDY 240  
Db 181 SRNNAQVLLPTFAQANVQLLLRLDQVYKQWPFPLSAENVRSSELISPNSGCDPTGDY 240  
  
QY 241 YERLKCKTAETNYCLYQVGLNQIKQGGTGADTWSKFNKFRREMTLAVLDIIAIFPTY 300  
Db 241 YERLKCKTAETNYCLYQVGLNQIKQGGTGADTWSKFNKFRREMTLAVLDIIAIFPTY 300  
  
QY 301 DFEKYPPLTHVELTREIYTDVAGVSSGYISWLRNWPNTFNGLEANGTRGPGVLVTWLSKIG 360

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Db 223 -----YPQNDIDL---FYKEQVSVTARYSDHCVQYNAGLNKLR--GTGAKQWV 266  
QY 278 KFNKFRREMTLAVLDDIIAIPPTDFEKYPLPHTVELTREIYTDVAG-YSSGTYSWLRNWP 336  
Db 267 DYNRFRREMNVMVLDLVALFPNDARYPLETNAELTREIFDPVGSYVTGQSSTLISWY 326  
QY 337 N-----TFNGLEANGTRGPGVLWLSKIGIYNEY----VSRVFAGWVGRHYEDYTKG 385  
Db 327 DMIPAAALPSPSTLE-NLRRPDPFTLLQEIWMYTSFRQNGTIEYNYWGGQRLTLSYIYG 385  
QY 386 NGIFQRMGTTSNDLRNIDFQNAADVYKI-----TSLAIMNLVGETTAR 428  
Db 386 SS-FNKYSGVLAGAEDIIPVGQNDIYRVVWYIIGRYTNSLLGVNPTVFYFSNNTQKTSK 444  
QY 429 PEY---RVSKADFRVCGPDI---NYDAGNGLSRMT---IESTFPLVLHSGNVGRGPSHR 479  
Db 445 PKQFAGGIKTID-----SGBELTYENQSYSHRVSYITSFEIKSTGGTVL---GV----- 491  
QY 480 LSNAACVVYGNRVNVYGVWTHTSIKRENIIEANQITQIPAVKSYYLQNYLANAYTVYIKG 539  
Db 492 -----VPIFGWTHSSASRNNFIYATKISQIPINKA---SRTSGGAVWNFQEG 535  
QY 540 THTGGDLIRELRTKSEYNAYAGG-----IRLIINNKTAGQSYRIRFRYAADKAAFFSV 594  
Db 536 LYNGGPVMKL-----SGSGSQVINLRVATDAKGASQRYRIRIRYASDRACKFTI 584  
QY 595 YLYPGGWSNRFVSLEKSYSGNY-----DDLKYSDPKFAEITTPPLPSSNIQMDVE 645  
Db 585 -----SSRSPENPATYSASIAYTNTMTSNASLTYSTPAYAE-----SGPINLGIS 629  
QY 646 MQANSFQSDV-----NVVLDKIEFLPSNTTILEYEGEDLEKTKNANDLFTN 693  
Db 630 GSSRTFDISITKEAGANLYIDRIEIPVNTL---FEABEDLDVAKAVNGLFTN 681

Search completed: December 15, 2005, 11:15:12

Job time : 193 secs

XX WPI: 1993-076511/09.  
 DR N-PSDB; AAQ36866.  
 XX  
 PT New strain of *Bacillus thuringiensis* serovar japonensis - producing toxin  
 PT active against coleoptera larvae.  
 XX  
 PS Claim 5; Page 28; 48pp; English.  
 XX  
 CC The protein sequence is that of a toxin active against Coleoptera that is  
 CC produced from a pure culture of *Bacillus thuringiensis* serovar japonensis  
 CC variety Buibui (FERM BP-3465). The toxin is a delta-endotoxin which has a  
 CC mol. wt. of ca. 130 kD. It is useful for control of coleoptera larvae  
 CC e.g. it is effective against *Anomala cuprea* but has little effect on  
 CC Lepidoptera. The toxin can be used as B.t. spores or crystals, as opt.  
 CC treated cells (B.t. or transformed microorganisms) or it is expressed by  
 CC plants. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-  
 CC 2003 to standardise OS field)  
 XX  
 SQ Sequence 1149 AA;

Query Match 19.9%; Score 728.5; DB 2; Length 1149;  
 Best Local Similarity 29.9%; Pred. No. 1.3e-48;  
 Matches 232; Conservative 124; Mismatches 240; Indels 179; Gaps 34;  
 QY 4 MSPYONKNEYELLESSNNNTTPN--RYPFANNRDMSTMWDCOGISWDE----- 52  
 DB 1 MSP-NNQNEYELIDALSPSVSDNSIRYPLANDQNTLQNMNYKDYLNKTESTNAELSRN 59  
 QY 53 --IMESVETITSGINLIEFVIE---PSLGGINTLL-SIIGKLIPTNRQTVSALSICDL 105  
 DB 60 PCTFISAQDAVGTGIDIVSTIISGLGIPVLGEVFSILGSLGLWPSNNENWQIFMNRV 119  
 QY 106 LSIIRKEVADSVLSDAIADFDGKLKNYR---EYLSYLGAWLKDGKPKQKTNNSDIGQLV 162  
 DB 120 BELIDQKILDSVRSRAIAD---LANSRIAVEYQNALEDWRKNP---HSTRSAAL---- 168  
 QY 163 YFVKLSERDFN--ETLG---GSLSRNNAQVLLPTFAQANVQLLLRDAVQKQWPPF 217  
 DB 169 -----VKERFGNAELRTNMGSFSQNTYETPLPTIAQASLHLLVMDVQIYKEWG-- 222  
 QY 218 LSAENVRSSELISPNSCGDFTGDIYERLCKTAETNYCLYWTQVGLNQIKQGGTGADTWS 277  
 DB 223 -----YFQNDIDL--FYKEQVSYTARYSDHCQVQWYNAGLNKLR--GTGAKQWV 266  
 QY 278 KENKREMTLAVLDIIAIPFYDEKYPPLTHVELTRIIYTDVAG--YSSGYVSWLRNWP 336  
 DB 267 DYNRRFRNMVMDLVALFPNDYDARIYPLETNAELTREIFTDPVGSYVTGQSSTLISWY 326  
 QY 337 N-----TFNGLEANGTRGPGIATWLSKIGIYNEY---VSRYPAGWVGRHYEDYTKG 385  
 DB 327 DMIPALPSPSTLE-NLLRKPDPFTLLQBEIRMTSFRQNGTIEYNYWGGQLTSLYVG 385  
 QY 386 NGIFORMSGTNSLNRNIDFNADVYKI-----TSLAIMNLVGETTAR 428  
 DB 386 SS-FNKYSGLAGAEDIIPVGQNDIVRVVTVYIGRVYTNLSLLGVNVPVTFYSNNTQKYSK 444  
 QY 429 PEY---RVSKADFRVGGPDL---NYDAGNGLSRMT---ISTPLVLHSGVNGRPSHR 479  
 DB 445 PKQFAGGIKTID-----SGEELTYENQSYSHRVSYITSPFISKSTGTGTVL---GV----- 491  
 QY 480 LSNAACVVYGNRVNRYGWTHTSLKRENIIEANOLTOIPAKVSYLYQLNANAYTVVYK 539  
 DB 492 -----VPFQTHSASRNFIYATKISQIPINKA---SRTSGGAVNFPQEG 535  
 QY 540 THTGDLIRFLRTKSEYNVAYAGG-----IRLIINNTAGOSYRIRFRYAADKAAFFSV 594  
 DB 536 LYNQGPVVKL-----SGSGQVINLRVATDAKQASQYRIRIRYASDRAGKPTI 584  
 QY 595 YLPGWGNRFRVLSLEKSYSGNY-----DDLKYSDFKFAEITPPLPSNMQMOVE 645  
 DB 585 -----SSRSPENPATYSASIAVTNTMTSTNASLTYSTFYAE-----SCPINLGIS 629

QY 646 MQANSFQSDV-----NVVLDKLEPLSPNTTLEYEGERDLEKTKNVDLFTN 693  
 DB 630 GSSRTFDISITKEAGANLYIDRIEPIPVNTL---FEABEDLVAKKAVNGLFTN 681  
 RESULT 15  
 AARS1692  
 ID AARS1692 standard; protein; 1149 AA.  
 XX  
 AC AARS1692;  
 XX  
 DT 16-OCT-2003 (revised)  
 DT 04-NOV-1994 (first entry)  
 XX  
 DE B.thuringiensis serovar Japonensis insecticidal protein.  
 XX insecticidal protein; Coleoptera larvae; Buibui fungus.  
 XX  
 OS *Bacillus thuringiensis*; (serovar Japonensis).  
 OS strain Buibui).  
 XX  
 FH Key Location/Qualifiers  
 FT Region 751..766  
 FT /note= "amino acids 751-766 are not given in the  
 FT specification and so have been decoded from AAQ58975"  
 XX  
 JP06065292-A.  
 XX  
 PD 08-MAR-1994.  
 XX  
 PF 11-AUG-1992; 92JP-00213886.  
 XX  
 PR 11-AUG-1992; 92JP-00213886.  
 XX  
 PA (KUBI ) KUBOTA CORP.  
 XX  
 DR WPI: 1994-121220/15.  
 DR N-PSDB; AAQ58975.  
 XX  
 PT Insecticidal protein and DNA from *Bacillus thuringiensis* serovar  
 PT Japonensis strain Buibui - useful in insecticides against Coleoptera  
 PT insects.  
 XX  
 PS Claim 1; Page 9-13; 18pp; Japanese.  
 XX  
 CC This insecticidal protein has activity against Coleopteran insect larvae  
 CC and has been isolated from *Bacillus thuringiensis* serovar japonensis  
 CC strain Buibui. (Updated on 16-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 1149 AA;

Query Match 19.9%; Score 728.5; DB 2; Length 1149;  
 Best Local Similarity 29.9%; Pred. No. 1.3e-48;  
 Matches 232; Conservative 124; Mismatches 240; Indels 179; Gaps 34;  
 QY 4 MSPYONKNEYELLESSNNNTTPN--RYPFANNRDMSTMWDCOGISWDE----- 52  
 DB 1 MSP-NNQNEYELIDALSPSVSDNSIRYPLANDQNTLQNMNYKDYLNKTESTNAELSRN 59  
 QY 53 --IMESVETITSGINLIEFVIE---PSLGGINTLL-SIIGKLIPTNRQTVSALSICDL 105  
 DB 60 PCTFISAQDAVGTGIDIVSTIISGLGIPVLGEVFSILGSLGLWPSNNENWQIFMNRV 119  
 QY 106 LSIIRKEVADSVLSDAIADFDGKLKNYR---EYLSYLGAWLKDGKPKQKTNNSDIGQLV 162  
 DB 120 BELIDQKILDSVRSRAIAD---LANSRIAVEYQNALEDWRKNP---HSTRSAAL---- 168  
 QY 163 YFVKLSERDFN--ETLG---GSLSRNNAQVLLPTFAQANVQLLLRDAVQKQWPPF 217  
 DB 169 -----VKERFGNAELRTNMGSFSQNTYETPLPTIAQASLHLLVMDVQIYKEWG-- 222  
 QY 218 LSAENVRSSELISPNSCGDFTGDIYERLCKTAETNYCLYWTQVGLNQIKQGGTGADTWS 277



Db 190 IGTIVSLITAPSLTGLISIVYDLIGKVLGGSGQSISDLISICDLLSIIDLRVSQVLND 249  
 Qy 121 ATADFGKLVNREYVSLVGLAWLKGKPLQKTNNSDQGVYVYFKLSERDNEIL----- 176  
 Db 250 GIADFGSVLLYRN-VLEALDSWKN-----PNSASABELTRFRIADSEFDRLITRGS 302  
 Qy 177 ---GGSLRNNAQVLLPTFAQANVQMLLLDRDAVQYKAQW-----FPFLSAENVRSELI 228  
 Db 303 LINGGSLARNAQVLLPTFAQANVQMLLLDRDAVQYKAQW-----FPFLSAENVRSELI 362  
 Qy 229 SPNSGCDFTGDYERLCKTAYTNYCLVYQVGLNQIKQGGTGADTWSKFNKFRREMTL 288  
 Db 363 E-----LYDYCVHWYNGRGNELRQRTGSATAWLEFHYRREMTL 402  
 Qy 289 AVLIIAIPPTDFEYKPLPHTVELTREIYTTAVGY-----SSGTYSWLR--NWPYTFNGL 342  
 Db 403 MWLDIVASFSDDLITNYPIETDFQLSRVITDPIGFVHRSSLRGSEWFSFVNAN--FSDL 461  
 Qy 343 EANGTRGPGVLVWLSKIGIYNEVSRFAG-----WVGTREYEDYTKGNGIFORMSGT 395  
 Db 462 E-NAIPNRPSPFLNMMIISTGSLTLPVSPSTDRARVWYGSRRDISPANSQFTELISQ 520  
 Qy 396 TSNLRNIDFQNAVYKITSLAIMNLVGETTARPEYRVSKADPRRVGGPDLNADGNGL 455  
 Db 521 HTATQITILGRN--IPRVDQA-CNL-NDTT-----YGVNRAVF-----YHDASEG 563  
 Qy 456 SRMTSTPFLVHNSVGRP-----SHRLSNAACVVYV----- 489  
 Db 564 QRSVYEG-----YRTGIDNPRVQNTYLPGENSDIPTPDYTHILSTINLTGGLRQV 619  
 Qy 490 ---NSRVNVYGTWTSKRENIIEANQITQIPAVKSYVLYQNLVNAVYTVIKGTHGTD 545  
 Db 620 ASNRSSLVYVWYKTHSLARNNTINDRITQITPLK-----VTRGTGVSYNDPQFIGA 675  
 Qy 546 LIRFLRTKSEYNAVYAGGIRLIINNKTAGQSYRIRFRIAADKAFAFFSVLYPFGWGNR 605  
 Db 676 LLQ-----RTDHGSL-----GVLRVQPLHLRQYRIRVYASTNIRLSV-----NGS 719  
 Qy 605 FVSLKSYSGNY-----DDLKYSDFKAEIITPPLP--SSNTQMDVEWQANSFQSDVNVLDK 661  
 Db 720 FETISQNLPSMRLGDLRYGSAIRFNTSIRPTASPDQIRLTIEPSFIQEVYV--DR 777  
 Qy 662 IEFLPSNTTLEVEGERDELEKTKNAVNDLFT 692  
 Db 778 IEFIPVNPTR---EAKEDLEAKKAVASLFT 805  
 RESULT 12  
 AAW06417  
 ID AAW06417 standard; protein; 1169 AA.  
 XX AC AAW06417;  
 DT 16-OCT-2003 (revised)  
 DT 28-JAN-1997 (first entry)  
 DE Antiscarab pest toxin 50C(b).  
 XX KW Toxin 50C(b); scarab pest; toxin; insect; scarabaeidae; pest control;  
 KW larval stage insect; grain; tuberous crop; white grub; chafer grub;  
 KW cyclocephala; popillia.  
 XX OS Bacillus thuringiensis; strain kumamotoensis.  
 XX PN US5554534-A.  
 XX PD 10-SEP-1996.  
 XX PF 30-SEP-1994; 94US-00315468.  
 XX PR 16-DEC-1991; 91US-00808316.  
 PR 30-JAN-1992; 92US-00828430.  
 PR 01-FEB-1993; 93US-00014941.

XX (MYCO ) MYCOGEN CORP.  
 XX PA Focerrada L, Narva KE, Michaels TE;  
 PI N-PSDB; AAT43221.  
 DR WPI; 1996-424659/42.  
 XX N-PSDB; AAT43221.  
 PT New nucleic acid encoding B.thuringiensis toxin active against scarab(s)  
 PT - also related toxin and transformed microbes, effective against adult  
 PT pests and their larvae.  
 XX Claim 2; Col 29-36; 24pp; English.  
 XX AAW06417-W06419 represent toxins that are active against scarab pests.  
 CC The DNA encoding this sequence was isolated from the Bacillus  
 CC thuringiensis strain kumamotoensis. Insects in the family Scarabaeidae  
 CC constitute a serious pest control problem, especially when destructive  
 CC larval stage insects infest high value turf found in golf courses,  
 CC playing fields and lawns. The larvae of many species also attack grains,  
 CC tuberous crops, and ornamentals. The larvae are known as white grubs, or  
 CC chafer grubs, and can be found in decaying organic matter, or in the soil  
 CC where they consume plant roots. In Europe and the U.S. populations of  
 CC these larvae and adults have developed resistance to chemical  
 CC insecticides such as the organochlorines and DDT. These toxin sequences,  
 CC and intact cells that are capable of expressing these proteins, can be  
 CC used to control many pests of the family scarabaeidae, such as species of  
 CC Cyclocephala, and Popillia. The toxins are active against larvae (present  
 CC in soil) and against adults. (Updated on 16-OCT-2003 to standardise OS  
 CC field)  
 XX SQ Sequence 1169 AA;  
 Query Match 20.4%; Score 745; DB 2; Length 1169;  
 Best Local Similarity 29.4%; Pred. No. 6.6e-50;  
 Matches 217; Conservative 142; Mismatches 274; Indels 104; Gaps 31;  
 Qy 4 MSPQNKNEYEILES--SSNNTNTNRYPPAN--NRDMSTWSWDCQGIS-----W 50  
 Db 1 MSP--NNQNEYIIDIATPSTSVNSNRYPPANEPTNALQNDYDKDYLKMSAGNVSEYPGS 59  
 Qy 51 DEIVESVTITSIGINLIEFVIE-----PSLGGINTLLS-IIGKLIPTNROTYSALSICDL 105  
 Db 60 PEVFLSEQDAKAAIDIVGKLTGCVFVGPVIVSLYQLDILWPSQKSWBIFMEQV 119  
 Qy 106 LSIIRKEVADSVLSDAIDFDPKLVNRYEYLSYLGAWLKD---GKPLQKTNNSDIGQLV 162  
 Db 120 BELINQKIAEVARNKALSELEGLGNNY-QVLYTALKEENKPNPGRSALRDVNR----- 172  
 Qy 163 YPFKLSERDFNEILGSLSRNNAQVLLPTFAQANVQMLLLDRDAVQYKAQWFPFLSABN 222  
 Db 173 ---FEILDSLFTQYM-PSFRVTNFEVFPFLTVYTMANLHLLLRDASIFGEEM--GLSTST 227  
 Qy 223 VRSELI SPNSGCDFTGDYERLCKTAYTNYCLVYQVGLNQIKQGGTGADTWSKFNK 282  
 Db 228 I-----NNYINRQMKLTAEYSDHCVKWYETGLAKLK--GSSAKQWIDYNOF 271  
 Qy 283 REMTLAVLDIIAIPPTDFEYKPLPHTVELTREIYTTAVGYSS--GTYSMLRNWNPNTFN 340  
 Db 272 RREMTLTVLDVVAFPSNVDTRTYPLATTQAQLTREYVTDPLGAVDVPNIGSWYDKAP-SFS 330  
 Qy 341 GLEANGTRGPGVLVWLSKIGIYNEVVS-----RYFAGWVGTREHYEDYTKGNGIFORMSGTT 396  
 Db 331 EIEKAAIRPPHFVDYITGLTVYTKRSTSDRYMYWAGHQISYKHIGTSTSTFTQMYGTN 390  
 Qy 397 SN--DLRNIDFONADVYKITS--LAIMNLVGETTARPEYRVSKADFRVVG-----GPDLN 447  
 Db 391 QNLQSTSNFDTNVDIYKILNSGAVLLDIVPGYTYTFFGMPETEFPMVNLNTRKTLT 450  
 Qy 448 YDAGNNGLSRMTIESTFPLVLHNSG---VRGFSHRLSNAACVVYVGNR---YNYVGTWHT 501  
 Db 451 YKPASKDIIDTRDSELELPETSQPNVESYSHRLGHT-FIYSSSTSTYVVPFSWTHR 509



Qy	606	FVSLKSYSGNY---DOLKYSDFKFAIITPPLP-SSNIQMDVEMQANSFQSDVNVLDK	661
Db	592	FOTISQNLPMSTWGLGEDLRVSGFAIREFNFSIRPTASPDQIRLTIBPSFIRQEVVY--DR	649
Qy	662	IEFLPSNTTILEYEGERDLEKTKNAVNDLFT	692
Db	650	IEFIPVNPTR---EAKEDLEAKKAVASLFT	677
RESULT 9			
ID	AYY24959	standard; protein; 1156 AA.	
XX	AYY24959;		
DT	09-SEP-1999	(first entry)	
DE	Bacillus thuringiensis toxin 86BB1(a).		
KW	Bacillus thuringiensis; toxin; Ostrinia nubilalis; lepidopteran;		
XX	European corn borer; black cutworm.		
OS	Bacillus thuringiensis.		
PN	WO9933991-A2.		
PD	08-JUL-1999.		
PF	15-DEC-1998; 98WO-US026585.		
XX	31-DEC-1997; 97US-00002285.		
PR	(MYCO ) MYCOGEN CORP.		
PI	Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;		
PI	Muller-Cohn J;		
DR	WPI; 1999-405513/34.		
XX	N-PSDB; AAX83876.		
PT	Method for control of European corn borer using Bacillus thuringiensis		
PT	toxins.		
XX	Claim 1; Page 86-90; 174pp; English.		
XX	A method has been developed for the control of European corn borer		
CC	(Ostrinia nubilalis), comprising contacting the pest with a pesticidal		
CC	amount of a Bacillus thuringiensis toxin. The method is used for the		
CC	control of European corn borer (Ostrinia nubilalis). The method can also		
CC	be used for the control of other non-mammalian pests, particularly black		
CC	cutworm, and other lepidopteran pests. The present sequence represents a		
CC	Bacillus thuringiensis toxin from the present invention		
SQ	Sequence 1156 AA;		
Query Match 20.4%; Score 747; DB 2; Length 1156;			
Best Local Similarity 30.6%; Pred. No. 4.5e-50;			
Matches 230; Conservative 130; Mismatches 249; Indels 142; Gaps 31			
Qy	9	NKVEYIEILLESSNNTNTPN--RYFPANNRDMSTWNSDCQG---ISW-DEIWESVETITTS	62
Db	2	NONKHGIIIGASNCGCASDVAKYPLANNPYSSALNLNSCONSLIWNIIIGDAAKEAVS	61
Qy	63	IGINLIEFVIPSICGG-INTLLSIIGKLI-PTNRQTVSALSI CDLLSIIRKEVADSVLSD	120
Db	62	IGTTIVSLITAPSLTGLISIVYDLIGKVGSSQGISDLSI CDLLSIIDLRSVQSVLMD	121
Qy	121	ATAFDQGLKNRYEYLLSYLGAWLKDQKPLQKTNNSDIGLVYVFKLSERDFNEIL----	176
Db	122	GIADFNQSVLLYRN-YLEALDSWNKN-----PNSASAEELRTFRFRIADSEFDRLITRGS	174
Qy	177	---GGSLRRNAQVLLLLPTFAQANVOLLRLRDVAQVYKAQW-----FPFLSARNVRSELI	228



PR 20-FEB-2003; 2003US-0448810P.  
 PR 20-FEB-2003; 2003US-0448812P.  
 PR 19-FEB-2004; 2004US-00781979.  
 PR 19-FEB-2004; 2004US-00782020.  
 PR 19-FEB-2004; 2004US-00782096.  
 PR 19-FEB-2004; 2004US-00782141.  
 PR 19-FEB-2004; 2004US-00782570.  
 PR 19-FEB-2004; 2004US-00783417.  
 XX  
 PA (ATHE-) ATHENIX CORP.  
 XX  
 PI Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;  
 XX WPI; 2004-635574/61.  
 XX  
 DR New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
 PT for producing organisms with pesticide resistance.  
 XX  
 PS Example 6; SEQ ID NO 47; 178pp; English.  
 XX  
 CC This sequence represents a delta-endotoxin crystal protein. This protein  
 CC was included in the scope of the invention as a comparison to the delta-  
 CC endotoxins of the invention. Some of the delta-endotoxin coding sequences  
 CC of the invention have alternative start codons, producing more than one  
 CC protein from a single open reading frame. The nucleic acid sequences of  
 CC the invention are useful in DNA constructs or expression cassettes for  
 CC transformation and expression in plants and bacteria. The nucleic acids  
 CC and corresponding polypeptides are useful for killing lepidopteran or  
 CC coleopteran pests. Compositions containing the delta-endotoxins of the  
 CC invention, and methods for their production, are useful for the  
 CC production of organisms with pesticide resistance, specifically bacteria  
 CC and plants. These organisms are useful for generating altered or improved  
 CC delta-endotoxin or delta-endotoxin-associated proteins that have  
 CC pesticidal activity, or for detecting the presence of delta-endotoxin or  
 CC delta-endotoxin-associated proteins or nucleic acids in products or  
 CC organisms.  
 XX  
 SQ Sequence 674 AA;

Query Match 22.7%; Score 831; DB 8; Length 674;  
 Best Local Similarity 31.9%; Pred. No. 3.9e-57;  
 Matches 236; Conservative 131; Mismatches 257; Indels 116; Gaps 31;

QY 4 MSPYQNKNEYEILESSNNNTNTPRYPPANN-----RDMTMSW-NDCOG--ISWDEIWE 55  
 DB 1 MNOYQNKNEYEILESSNNMNPNNPPFADPNAMKNGNYKDWYNECEGNSIPSPAAA 60  
 QY 56 SVETITSGINLIEFIEPISLGGINTLISIGKLIPTNRQTVSALSICDLSIRKEVAD 115  
 DB 61 ITSKIVSIVLTKAKAVASSLA--DSIKSLGISKITTENNVSQVMVQVHQIINRTOE 118  
 QY 116 SVLSDAIADFDGKLNRYEYLSYLGAMUKGKPKLOKTNNSDIG---QLVYVFKLSERDF 172  
 DB 119 TILDGESSLGLVAIYNRDYLGALEAW-----NNKSNINYQTNVAEAFKTVREF 170  
 QY 173 NEILGSSLRNNAQVLLPTFAQANVQLLLARDVAOVYKAQWFFLSAENVESELISPS 232  
 DB 171 FTKLGIYRTSSQITLPTFTQAANLHLSMLRDVAMYQEGW-----NLQSHI----- 218  
 QY 233 GCDFTGDYVERLKCKTAETNYCLWYQVGLNQIKQGGTGADTKSKFNKFRREMTLAVLD 292  
 DB 219 -----NYSKELDDALEDTNYCEVYTKGLNALR-GSTAID-WLEFNSFRDMLTAVLD 270  
 QY 293 IIAIPTDYDEKYPPLTHVELTREIYTDAGVSSGTYSWLRNWPNT-----FNGLEANG 346  
 DB 271 LVAIFPNYNPVRYPLSTKLSRKIYTDVGRDTSPLS--FGDWTNTGRTLANFNDLREV 328  
 QY 347 TRGRGLVTLWSKIGLYNEVSYR-----FAGVGTGTHYEDYT-KNGNIFQRMSCGT- 396  
 DB 329 TUSPSLVKWLGMQMTIYTGDAISYRPTSPGDRIGWYGNINAFYHGTGRTDVMFROGTDA 388  
 QY 397 ----SNDLRNIDFQNAVYK--ITSLAIMNLVG--ETTARPEYRVSKADFRVRGVPDLNY 448

DB 389 YEDSTFISNLYD--DIYKLDLRAAAVSTTQGMDDT-----FGVSSSRFFDIRGRNOLY 442  
 QY 449 DAGNNGLSRMTTESTFPLVLHNSG-VRGPSHRL-----SNAACVVYGNRNVYVYGWTH 500  
 DB 443 QS-NKPYPSLPITITTPGEESESGNANDYSHLLCDVKILQEDSSNICGRSSLLSHAWTH 501  
 QY 501 TSLAKRENIIEANQITQIPAKSVYLYONLANAYTVIKGT-HTGGDLIRFLRTKSEYNVAV 559  
 DB 502 ASLDRNNTILPDEITQIPAVTAYELR-----GNSSVAGPGSTGGDLV-----KMSYHSV 551  
 QY 560 YAGGGIRLIINNKTAGQSYRIRFRYAADKAAFF-----SVLYPGGWSNRFVSLEKSY 613  
 DB 552 WS---FKYVCSEL---KNYRVIRYASHGNCQFLMKRWPTGVAPQWARRH---NVQGTG 602  
 QY 614 SGNVDDLKYSFKFAEIIITPPLPSNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTLE 673  
 DB 603 S---NSMRYEAFKVLIDFTITPEENNFAFTIDLESGG-----DLFDIKIEFTPVSGSAFE 654  
 QY 674 YEGERDLEKTKNAVNDLFTN 693  
 DB 655 YEGQNIEKTKQAVNDLFIN 674

RESULT 7  
 ID AEA81457 standard; protein; 1151 AA.  
 XX AEA81457;  
 XX 25-AUG-2005 (first entry)  
 DE Bacillus thuringiensis Cry9 protein, cryaa2, SEQ ID NO: 13.  
 KW Transgenic plant; pesticide; genetically engineered microorganism; cry9;  
 KW endotoxin.  
 XX Bacillus thuringiensis.  
 XX US2005138685-A1.  
 XX 23-JUN-2005.  
 XX 21-DEC-2004; 2004US-00018615.  
 XX 22-DEC-2003; 2003US-0531807P.  
 XX (DUPO) DU PONT DE NEMOURS & CO E I.  
 XX Flannagan RD, Abad AR;  
 XX WPI; 2005-444221/45.  
 XX  
 PT New isolated nucleic acid encoding a polypeptide having pesticidal  
 PT activity, useful for controlling pests, especially plant pests such as  
 PT European corn borer, diamond-back moth or fall armyworm.  
 XX Disclosure; SEQ ID NO 13; 114pp; English.  
 XX  
 CC The present invention relates to the Bacillus thuringiensis Cry9-family  
 CC genes that encode delta-endotoxins having pesticidal activity against  
 CC insect pests. The invention is useful for producing pesticidal  
 CC compositions for controlling pests in plant such as European corn borer,  
 CC diamond-back moth or fall armyworm. The invention is also useful in  
 CC production of transgenic plant. The present sequence is the Bacillus  
 CC thuringiensis Cry9 protein.  
 XX Sequence 1151 AA;

Query Match 20.4%; Score 747; DB 9; Length 1151;  
 Best Local Similarity 30.6%; Pred. No. 4.4e-50;  
 Matches 230; Conservative 130; Mismatches 249; Indels 142; Gaps 31;

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RESULT 5
ADR89417
ID ADR89417 standard; protein; 669 AA.
XX
AC ADR89417;
XX
DT 18-NOV-2004 (first entry)
XX
DE AXMI-008 alternative protein.
XX
KW delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX
OS Bacillus thuringiensis.
XX
PN WO2004074462-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX
PA (ATHE-) ATHENIX CORP.
XX
PI Carozzi N, Hargise T, Koziel MG, Duck NB, Carr B;
XX
XX WPI; 2004-635574/61.
DR N-PSDB; ADR89416.
XX
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
XX Claim 12; SEQ ID NO 29; 178pp; English.
XX
XX This sequence represents an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX
SQ Sequence 669 AA;
Query Match 42.7%; Score 1561.5; DB 8; Length 669;
Best Local Similarity 47.1%; Pred. NO. 1.6e-115;
Matches 338; Conservative 107; Mismatches 197; Indels 75; Gaps 18;
XX
4 MSPYQKNVEYILESSNNNTNPNRYPFANNRDMSTMWDCQIGSWDIWESVETITSI 63
XX 1 MNSYQNTNEYIILDGSPNNMNSRYPFAKDPNIPFNILDACQGRPQDTWESVDIVTI 60

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QY 64 GINLIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLSIIRKEVADVSLSDAIA 123
DB 61 GTYLIOFLLEPGIGGIPVIFSIINKLIPSSGQVAALSICDLVSIIRKEVDESVLSDGVA 120
QY 124 DFDGKLKNRYEYLSYLGAWLKDGPLOKLTNNSDIGOLVYVFKLSERDRNEILGGSLSRN 183
DB 121 DFEGETAYQDYLYLHYLEDWLT-----KSNPKKLADVVVKQFQAREEDFTKLAGLSURQ 175
QY 184 NAQVLLPTFAQAANVQLLLRDVAQYKAQWEPFLSAENVRSSELISNSGCDFTGDIYER 243
DB 176 KAEILLPTVQAANVHLLLRDAVYKKEW-----GLVCPPLYPGSG---RTDCNER 225
QY 244 LKCKTAETNYCLYWTQVGLNQIKQGTGADTWKSKFNKFRREMTLAVLDIIAIPPTVDPE 303
DB 226 LKAKIKEYTNYCVGWTNKGDLQIQAGTSAEVMKSKFNKFRREMTLAVLDIIAIPPTVDPE 285
QY 304 KYPLPHVELTREIYTDVAGYSGTYSWLRNPNPTENGLEANGTRGPGVLTWLSKIGIYN 363
DB 286 KYPLATSVELTREIYTDVPVYSGNGYGERFP--SFNSVEANGTRGPGVLTWLSKIGIYN 343
QY 364 EYVS---RYFAGWVGTRHYEDYTKNGIFQRMSTGTTSDNLRNIDFQNAVYKITSL---A 417
DB 344 HSINLQLGLYSGWGGTRHYEDFTKNGAFQRMSTGTTSDNLRNIDFQNAVYKITSL---A 403
QY 418 INNLVGETTARPEYRVSKADFRVVGPDNLNYDAGNGLSRMTIESTFPLVLHSGNVR--- 474
DB 404 MQPFVGYSI--PRHLVSRABEPFPTTLNTPLYEVNMSGYSQ--TIESVLP-----GINKDL 454
QY 475 -----GPHRLSNAACVVYGNRSRVNNGVWTHTSKRENIIEANQITQIPAVKSYLQNYL 529
DB 455 PPSRTNYSRLSNAACVQNETSRVNVFGWTHTSKRENIIEANQITQIPAVKSYLQNYL 514
QY 530 ANAYTVVIKGT-HTGGDLIRFLRTKSEYNNAVAGGIRLIINNKTAGQYRIRFRYAADK 588
DB 515 GVAGGYVTAGPGYTGDDVTL-----PYQA-----SLKIRLTSAPTNKYRVLRYASGG 564
QY 589 AAFPSVYLYPGWGNRFRVSLKSYSGNYDDLYKSDFKFAEITTPPLPSSNIQMDVEMQA 648
DB 565 PGFPRVERMSPSSVSN--ANFSRPATGG-----YSSFDYVDVTLVTTFNQSGVEIILQN-- 615
QY 649 NSFQSDVNVVLDKIRFLP-----SNTTILEYGE-----RDLEKTKNAVNDLFTN 693
DB 616 ---LSGYHLIVDKVEFIPIDIQIEKTKCQFEGDICRCEGVQSLETKEIVNSLFIN 669
RESULT 6
ADR89435
ID ADR89435 standard; protein; 674 AA.
XX
AC ADR89435;
XX
DT 18-NOV-2004 (first entry)
XX
DE cry24Aa.
XX
KW delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX
OS Bacillus thuringiensis.
XX
PN WO2004074462-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.

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363	VSRYPSGVGTRHYEDYITGNGNFORMSGTTSNDLDRISPNSGDI FKIESKAIMNVLGEI	422
Qy		
426	TARPEYRVSKADPRRVGGPDLDNYDAGNGLSRMTIESTPLVLHSGVRGP	478
Qy	: :	SH
423	NARPEYRVSRASFSESTAFIVLYDAGNSGLSMITISKLP	476
Db	: :	
479	RLSNAACVYVGNRVNVYGTHTSLKRNIIIEANQITQIPAKVSYLYQNLVLANAYTVVTK	538
Qy	: :	
477	RLSNAACVAGAGNSRINVYGTHTSMKNTLYPDKIQTQIPAVKAFDUSD	533
Db	: :	
539	GT-HTGGDDLIRFLRTKSEYNVAYGGGIRLIINNKTAGQSYRIFRYAADKAAFFSVYLY	597
Qy	: :	
534	GPCHTGCNVSL-----PYISRLKIRLI--PASTNKNLYVRVRYTSTS-----NGRELL	579
Db	: :	
598	PGCGWGNRRFVSLKESY-----SGNYDDLKYSDFKFAEIIPTPLPSSNIOMDVEMQANSFQ	652
Qy	: :	
580	VERWSPS-----SLINSIFPLPSGPGDSPGYVD-----TLVTFPQSGVBEIIQNLD	627
Db	: :	
653	SDVNVVLDKIEFLPSNTTLETYEGEDRLKTNKAVNDLFL	691
Qy	: :	
628	TPINV--DKVEPIPNVSTALRYEGKOSLEKADVVNDLFL	664
Db	: :	

## RESULT 4

RESULTS 4  
ADR89415  
ID ADR89415 standard: protein: 672 AA.

18-NOV-2004 (first entry)

AXMT-008

KW delta-endotoxin; delta-endotoxin associate polypeptide;  
 KW expression cassette; transformation; transgenic; plant;  
 KW lepidoptera; coleoptera; pest; pesticide; resistance;  
 KW pesticidal activity.

XX  
OS  
OS  
Bacillus thuringiensis.

Key	Location/Qualifiers
FH	

FT key Misc-difference 1

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FT      misc-reference 1
FT      /note= "Encoded by GTG"

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PN WO2004074462-A2

02-SEP-2004

XX  
PF  
20-FEB-2004. 2004WO-IIS005829XX  
PR 20-FEB-2003. 2003US-0448632D

PR 20-FEB-2003; 2003US-0448632P.  
PR 20-FEB-2003; 2003US-0448633P.  
PR 20-FEB-2003; 2003US-0448633P.

PR 20-FEB-2003; 2003US-0448633P.  
PR 20-FEB-2003; 2003US-0448797P.

PK Z0-FEB-2003; Z003US=0448797E;  
PB Z0-FEB-2003; Z003US=0448806P;

PK 20-FEB-2003; 2003US-0448806P;  
PR 20-FEB-2003; 2003US-0448810P;

20-FEB-2003; 2003US-0448812P.  
20-FEB-2003; 2003US-0448812P.  
20-FEB-2003; 2003US-0448812P.

PR 19-FEB-2004: 2004US-00781979.  
Z0-FEB-2003: 2003US-044881ZE.

19-FEB-2004; 2004US-00782020.

PR 19-FEB-2004; 2004US-00782096.

PR 19-FEB-2004; 2004US-00782141.

PR 19-FEB-2004; 2004US-00782570.

PR 19-FEB-2004; 2004US-00783417.

PA (ATHE-) ATHENIX CORP.

PI Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;

DR WPI; 2004-635574/61.

DR N-PSDB; ADR89413, ADR89414.

New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
PT for producing organisms with pesticide resistance.

QY 4 MSPQNKNEYEILESSNNTNTNRYPFANNRDMTSMWDCOGISWDEIWESVETITSI 63  
DB 1 MSPQNKNEYEILESSNNTNTNRYPFANNRDMTSMWDCOGISWDEIWESVETITSI 60  
QY 64 GINLIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLLSIIRKEVADSVLSDAIA 123  
DB 61 GINLIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLLSIIRKEVADSVLSDAIA 120  
QY 124 DFGKLNRYEYLSYLGAWLKDGPLOKTNNSDIGOLVYVYFKLSERDFNEIILGSLSRN 183  
DB 121 DFGKLNRYEYLSYLGAWLKDGPLOKTNNSDIGOLVYVYFKLSERDFNEIILGSLSRN 180  
QY 184 NAOVLLPTFAQANVOLLLLRDAVOYKAQWFFPFLSAENVRSELISPSNCCDFTGDYER 243  
DB 181 NAOVLLPTFAQANVOLLLLRDAVOYKAQWFFPFLSAENVRSELISPSNCCDFTGDYER 240  
QY 244 LKCKTAEYTYCLYQVGLNQIKQGGTGADTWSKFNKFRREMTLAVLDIIAIFPTDYFE 303  
DB 241 LKCKTAEYTYCLYQVGLNQIKQGGTGADTWSKFNKFRREMTLAVLDIIAIFPTDYFE 300  
QY 304 KYPLPHVELTREIYTDVAGYSSGTYSWLRNWPNTFNGLEANGTRGPGLVTLWSKIGIYN 363  
DB 301 KYPLPHVELTREIYTDVAGYSSGTYSWLRNWPNTFNGLEANGTRGPGLVTLWSKIGIYN 360  
QY 364 EYVSRYFAGWVGRHYEDYTKNGIIFORMSGTTSNDLRNIDFONADVYKITSIAINLVG 423  
DB 361 EYVSRYFAGWVGRHYEDYTKNGIIFORMSGTTSNDLRNIDFONADVYKITSIAINLVG 420  
QY 424 ETTARPEYRSKADFRVGGPDLYDAGNGLSRMTIESTFPLVLHNSVGRGSPSHLSNA 483  
DB 421 ETTARPEYRSKADFRVGGPDLYDAGNGLSRMTIESTFPLVLHNSVGRGSPSHLSNA 480  
QY 484 ACVYGNRNVYVGTWHTSLKRNIIIEANQITQIPAVKSYLQNYLANAYTVYIKGTHTG 543  
DB 481 ACVYGNRNVYVGTWHTSLKRNIIIEANQITQIPAVKSYLQNYLANAYTVYIKGTHTG 540  
QY 544 GDILRLFKTSEYNAVYAGGIRLIIINNKTAGOSYRIRFRYAADKAAFFSVLYPGWGS 603  
DB 541 GDILRLFKTSEYNAVYAGGIRLIIINNKTAGOSYRIRFRYAADKAAFFSVLYPGWGS 600  
QY 604 NREVSLEKSYSGNYDDLKYSDFKFABIIITPPLSSNIQMDVEMQANSFQSDVNVVLDKIE 663  
DB 601 NREVSLEKSYSGNYDDLKYSDFKFABIIITPPLSSNIQMDVEMQANSFQSDVNVVLDKIE 660  
QY 664 FLPSNTTILEYGERDLEKTKNAVNDLFTN 693  
DB 661 FLPSNTTILEYGERDLEKTKNAVNDLFTN 690

RESULT 3  
ADR89439

ID ADR89439 standard; protein; 666 AA.

AC ADR89439;  
XX ADR89439;

DT 18-NOV-2004 (first entry)  
DE cry40aa1.

KW delta-endotoxin; delta-endotoxin associate polypeptide;  
KW expression cassette; transformation; transgenic; plant; bacteria;  
KW lepidoptera; coleoptera; pest; pesticide; resistance;  
KW pesticidal activity.

OS Bacillus thuringiensis.  
XX

PN WO2004074462-A2.  
XX

XX 02-SEP-2004.  
XX

XX 20-FEB-2004; 2004WO-US005829.  
XX

XX 20-FEB-2003; 2003US-0448632P.  
PR

PR 20-FEB-2003; 2003US-0448633P.  
PR 20-FEB-2003; 2003US-0448797P.  
PR 20-FEB-2003; 2003US-0448806P.  
PR 20-FEB-2003; 2003US-0448810P.  
PR 19-FEB-2003; 2003US-0448812P.  
PR 19-FEB-2004; 2004US-00781979.  
PR 19-FEB-2004; 2004US-00782020.  
PR 19-FEB-2004; 2004US-00782096.  
PR 19-FEB-2004; 2004US-00782141.  
PR 19-FEB-2004; 2004US-00782570.  
PR 19-FEB-2004; 2004US-00783417.  
XX (ATHE-) ATHENIX CORP.  
XX  
XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;  
PI WPI; 2004-635574/61.  
XX  
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
PT for producing organisms with pesticide resistance.  
XX  
XX Example 6; SEQ ID NO 51; 178pp; English.  
XX  
CC This sequence represents a delta-endotoxin crystal protein. This protein  
CC was included in the scope of the invention as a comparison to the delta-  
CC endotoxins of the invention. Some of the delta-endotoxin coding sequences  
CC of the invention have alternative start codons, producing more than one  
CC protein from a single open reading frame. The nucleic acid sequences of  
CC the invention are useful in DNA constructs or expression cassettes for  
CC transformation and expression in plants and bacteria. The nucleic acids  
CC and corresponding polypeptides are useful for killing lepidopteran or  
CC coleopteran pests. Compositions containing the delta-endotoxins of the  
CC invention, and methods for their production, are useful for the  
CC production of organisms with pesticide resistance, specifically bacteria  
CC and plants. These organisms are useful for generating altered or improved  
CC delta-endotoxin or delta-endotoxin-associated proteins that have  
CC pesticidal activity, or for detecting the presence of delta-endotoxin or  
CC delta-endotoxin-associated proteins or nucleic acids in products or  
CC organisms.  
XX  
SQ Sequence 666 AA;

Query Match 63.7%; Score 2329.5; DB 8; Length 666;  
Best Local Similarity 67.2%; Pred. No. 6.4e-177;  
Matches 470; Conservative 62; Mismatches 116; Indels 51; Gaps 12;

QY 7 YONKNEYEILESSNNTNTNRYPFANNRDMTSMWDCOGISWDEIWESVETITSIGIN 66  
DB 3 YENKNEYEILESSNNTNPNRYPFANDRDMTSMFNDCCGISWDEIWESAETITSIGID 62  
QY 67 LIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLLSIIRKEVADSVLSDAIADF- 125  
DB 63 LIEFLMEPSLGGINTLFSIIGKLIPTNHQSVSALSICDLLSIIRKEVADSVLSDAICRFL 122  
QY 126 DGKLNRYEYLSYLGAWLKDGPLOKTNNSDIGOLVYVYFKLSERDFNEIILGSLSRNNA 185  
DB 123 DGKLNRYEYLPYLEAWLKDGPLOKTNNSDIGOLVYVYFKLSERDFNEIILGSLSRNNA 182  
QY 186 QVLLPTFAQANVOLLLLRDAVOYKAQWFFPFLSAENVRSELISPSNCCDFTGDYVERLK 245  
DB 183 QLLLPYFCASCCKQLLLLRDAVQYEEQWFFPFLSAENVRSELISPSNCCDFTGDYVERLK 242  
QY 246 CKTAEYTYCLYQVGLNQIKQGGTGADTWSKFNKFRREMTLAVLDIIAIFPTDYFEKY 305  
DB 243 CKIAEYTYCEYQAGLNQIKQAGTGADTWSKFNKFRREMTLAVLDIIAIFPTDYFKKY 302  
QY 306 PLPHTVELTREIYTDVAGYSSGTYSWLRNWPNTFNGLEANGTRGPGLVTLWSKIGIYNEY 365  
DB 303 PLPHTVELTREIYTDVAGYSSGTYSWLKYWTGAFNTLEANGTRGPGLVTLWSIGIYNEY 362  
QY 366 VSRYPAGWVGRHYEDYTKNGIIFORMSGTTSNDLRNIDFONADVYKITSIAINLVGSET 425

PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
 XX for producing organisms with pesticide resistance.

PS Claim 12; SEQ ID NO 14; 178pp; English.

XX This sequence represents an isolated delta-endotoxin. Some of the delta-  
 CC endotoxin coding sequences of the invention have alternative start  
 CC codons, producing more than one protein from a single open reading frame.  
 CC The nucleic acid sequences of the invention are useful in DNA constructs  
 CC or expression cassettes for transformation and expression in plants and  
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for  
 CC killing lepidopteran or coleopteran pests. Compositions containing the  
 CC delta-endotoxins of the invention, and methods for their production, are  
 CC useful for the production of organisms with pesticide resistance,  
 CC specifically bacteria and plants. These organisms are useful for  
 CC generating altered or improved delta-endotoxin or delta-endotoxin-  
 CC associated proteins that have pesticidal activity, or for detecting the  
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or  
 CC nucleic acids in products or organisms.

XX Sequence 693 AA;

Query Match 100.0%; Score 3655; DB 8; Length 693;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-283;  
 Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKMSPYQKNYEILESSNNTNPNRYPPANNRDMSTMSWDCQGISWDEIWSVETI 60  
 DB 1 MKKMSPYQKNYEILESSNNTNPNRYPPANNRDMSTMSWDCQGISWDEIWSVETI 60  
 QY 61 TSIGINLIEFVLEPSLGGINTLISIGKLIPTNROTVSALSICDLISIRKEVADSVLSD 120  
 DB 61 TSIGINLIEFVLEPSLGGINTLISIGKLIPTNROTVSALSICDLISIRKEVADSVLSD 120  
 QY 121 ATADFDGKLKNRYEYLSYLGAWLKDGPLOKTNNSDIGQLVYFKLSERDFNEILGSSL 180  
 DB 121 ATADFDGKLKNRYEYLSYLGAWLKDGPLOKTNNSDIGQLVYFKLSERDFNEILGSSL 180  
 QY 181 SRNNAQVLLPTFAAANVQLLLLRDAVQYKAQWFFLSAENVRSELISPSNGCDFTGDY 240  
 DB 181 SRNNAQVLLPTFAAANVQLLLLRDAVQYKAQWFFLSAENVRSELISPSNGCDFTGDY 240  
 QY 241 YERLCKTAETNYCLYQVGLNQIKGGTGADTWSKFNKPRREMTLAVLDIIAIFPTY 300  
 DB 241 YERLCKTAETNYCLYQVGLNQIKGGTGADTWSKFNKPRREMTLAVLDIIAIFPTY 300  
 QY 301 DFEKYPPLPHVELTREIYTDVAGYSSGTYSWLRNPNFTFNGLEANGTRGPGGLVTLWSKIG 360  
 DB 301 DFEKYPPLPHVELTREIYTDVAGYSSGTYSWLRNPNFTFNGLEANGTRGPGGLVTLWSKIG 360  
 QY 361 IYNEVYSRYFAGWGTGRHYEDYTKNGIFORMSGTSDNLRNIDFQNAVYKITSIAIMN 420  
 DB 361 IYNEVYSRYFAGWGTGRHYEDYTKNGIFORMSGTSDNLRNIDFQNAVYKITSIAIMN 420  
 QY 421 LVGETTAREYRVSKADPRRVGPDLYDAGNGLSRMTIESTFPLVHNSGVGPGSHRL 480  
 DB 421 LVGETTAREYRVSKADPRRVGPDLYDAGNGLSRMTIESTFPLVHNSGVGPGSHRL 480  
 QY 481 SNAACVYVNSRVNRYVGMTHTSKRENIIEANQITQIPAVKSYIYQLNYLANAYTVIKGT 540  
 DB 481 SNAACVYVNSRVNRYVGMTHTSKRENIIEANQITQIPAVKSYIYQLNYLANAYTVIKGT 540  
 QY 541 HTGGDLIRFLRTKSEYNAVAGGRLIINNTAGQSVIRIRYAADKAAFPVLYLPGG 600  
 DB 541 HTGGDLIRFLRTKSEYNAVAGGRLIINNTAGQSVIRIRYAADKAAFPVLYLPGG 600  
 QY 601 WGSNRFVLSLEKSYSGNYDCLKYSDFKFARIITPPLPSSNIQMDVEMQANSFOSDVNVVLD 660  
 DB 601 WGSNRFVLSLEKSYSGNYDCLKYSDFKFARIITPPLPSSNIQMDVEMQANSFOSDVNVVLD 660  
 QY 661 KIEFLPSTNTTLEYEGERDLEKTKNAVNDLFTN 693  
 DB 661 KIEFLPSTNTTLEYEGERDLEKTKNAVNDLFTN 693

Db 661 KIEFLPSTNTTLEYEGERDLEKTKNAVNDLFTN 693

# RESULT 2

ID ADR89404  
 AC ADR89404;  
 DT 18-NOV-2004 (first entry)  
 AXMI-008 alternative protein.

delta-endotoxin; delta-endotoxin associate polypeptide;  
 expression cassette; transformation; transgenic; plant; bacteria;  
 lepidoptera; coleoptera; pest; pesticide; resistance;  
 pesticidal activity.

Bacillus thuringiensis.

WO2004074462-A2.

02-SEP-2004.

20-FEB-2004; 2004WO-US005829.

20-FEB-2003; 2003US-0448632P.

20-FEB-2003; 2003US-0448633P.

20-FEB-2003; 2003US-0448797P.

20-FEB-2003; 2003US-0448806P.

20-FEB-2003; 2003US-0448810P.

20-FEB-2003; 2003US-0448812P.

19-FEB-2004; 2004US-00781579.

19-FEB-2004; 2004US-00782096.

19-FEB-2004; 2004US-00782141.

19-FEB-2004; 2004US-00782570.

19-FEB-2004; 2004US-00783417.

(ATHE-) ATHENIX CORP.

Carozzi N, Harglass T, Koziel MG, Duck NB, Carr B;  
 WPI, 2004-635574/61.  
 N-PSDB; ADR89403.

New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
 and polypeptides, useful for killing lepidopteran or coleopteran pests or  
 for producing organisms with pesticide resistance.

Claim 12; SEQ ID NO 16; 178pp; English.

This sequence represents an isolated delta-endotoxin. Some of the delta-  
 endotoxin coding sequences of the invention have alternative start  
 codons, producing more than one protein from a single open reading frame.  
 The nucleic acid sequences of the invention are useful in DNA constructs  
 or expression cassettes for transformation and expression in plants and  
 bacteria. The nucleic acids and corresponding polypeptides are useful for  
 killing lepidopteran or coleopteran pests. Compositions containing the  
 delta-endotoxins of the invention, and methods for their production, are  
 useful for the production of organisms with pesticide resistance,  
 specifically bacteria and plants. These organisms are useful for  
 generating altered or improved delta-endotoxin or delta-endotoxin-  
 associated proteins that have pesticidal activity, or for detecting the  
 presence of delta-endotoxin or delta-endotoxin-associated proteins or  
 nucleic acids in products or organisms.

Sequence 690 AA;

Query Match 99.6%; Score 3640; DB 8; Length 690;

Best Local Similarity 100.0%; Pred. No. 1.2e-281;

Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2005, 11:07:19 ; Search time 190 Seconds  
(without alignments)  
1602.576 Million cell updates/sec

Title: US-10-781-979-3

Perfect score: 3655

Sequence: 1 MKQSPYQNKVEVLELSSS.....YEGERDLEKTVKAVNDLFTN 693

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A\_Geneseq\_21.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*  
9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3655	100.0	693	ADR89402	Adr89402 AXMI-008.
2	3640	99.6	690	ADR89404	Adr89404 AXMI-008
3	2329.5	63.7	666	ADR89439	Adr89439 cry40Aa1.
4	1571.5	43.0	672	ADR89415	Adr89415 AXMI-008.
5	1561.5	42.7	669	ADR89417	Adr89417 AXMI-008
6	831	22.7	674	ADR89435	Adr89435 cry24Aa.
7	747	20.4	1151	Aea81457	Aea81457 Bacillus
8	747	20.4	1156	AAW46856	Aaw46856 Bacillus
9	747	20.4	1156	AAY24959	Aay24959 Bacillus
10	747	20.4	1156	AEA81456	Aea81456 Bacillus
11	747	20.4	1279	AAV82988	Aav82988 Native Cr
12	745	20.4	1169	AAW06417	Aaw06417 Antiscara
13	728.5	19.9	704	AAK51693	Aar51693 B.thuring
14	728.5	19.9	1149	AAK32354	Aar32354 Coleopter
15	728.5	19.9	1149	AAK51692	Aar51692 B.thuring
16	725	19.8	1167	AAU80281	Aau80281 Bacillus
17	724	19.8	659	ADR89437	Adr89437 cry39Aa.
18	724	19.8	1208	AAU02093	Aau02093 Bacillus
19	713.5	19.5	1206	AAU99235	Aau99235 Bacillus
20	713.5	19.5	1206	ADL15305	Adl15305 B.thuring
21	713.5	19.5	1206	AEb45607	Aeb45607 B.thurin
22	712	19.5	902	AAU02035	Aau02035 B.thurin
23	708.5	19.4	1227	AAV31990	Aav31990 Chimeric
24	707.5	19.4	719	ABB07073	Abb07073 Bacillus

25	707.5	19.4	719	9	ADY59880	Ady59880 Bacillus
26	707.5	19.4	719	9	ADY59881	Ady59881 Bacillus
27	705.5	19.3	1209	4	AAU02094	Aau02094 Bacillus
28	705.5	19.3	1228	9	ADY59858	Ady59858 Bacillus
29	703.5	19.2	652	3	AAV83039	Aay83039 Cry9Aa to
30	703.5	19.2	656	3	AAV83040	Aay83040 Synthesis
31	702.5	19.2	1228	2	AAK50955	Aar50955 Bacillus
32	700	19.2	710	4	AAU02041	Aau02041 B.thurin
33	699	19.1	1217	4	AAU02092	Aau02092 Bacillus
34	690.5	18.9	675	8	ADR89436	Adr89436 cry25Aa.
35	689	18.9	1227	2	AAW44321	Aaw44321 Bacillus
36	689	18.9	1227	4	AAU19950	Aab19950 Bacillus
37	686	18.8	1227	4	AAU02046	Aau02046 B.thurin
38	683	18.7	682	8	ADR89408	Adr89408 AXMI-009.
39	681	18.6	1186	2	AAV16796	Aay16796 Amino aci
40	681	18.6	1230	8	ADK98484	Adk98484 B.thuring
41	681	18.6	1230	8	ADK98489	Adk98489 B.thuring
42	681	18.6	1230	8	ADK98481	Adk98481 B.thuring
43	681	18.6	1230	8	ADK98491	Adk98491 B.thuring
44	681	18.6	1230	8	ADK98487	Adk98487 B.thuring
45	679	18.6	719	4	AAK66908	Aab66908 Insectici

## ALIGNMENTS

RESULT 1  
ADR89402  
ID ADR89402 standard; protein; 693 AA.  
AC ADR89402;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE AXMI-008.  
XX  
KW delta-endotoxin; delta-endotoxin associate polypeptide;  
KW expression cassette; transformation; transgenic; plant;  
KW lepidoptera; coleoptera; pest; pesticide; resistance;  
KW pesticidal activity.  
XX  
OS Bacillus thuringiensis.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1 /note= "Encoded by GTG"  
XX  
PN WO2004074462-A2.  
XX  
PD 02-SEP-2004.  
XX  
20-FEB-2004; 2004WO-US005829.  
XX  
20-FEB-2003; 2003US-0448632P.  
XX  
20-FEB-2003; 2003US-0448633P.  
XX  
20-FEB-2003; 2003US-0448797P.  
XX  
20-FEB-2003; 2003US-0448806P.  
XX  
20-FEB-2003; 2003US-0448810P.  
XX  
20-FEB-2003; 2003US-0448812P.  
XX  
19-FEB-2004; 2004US-00781979.  
XX  
19-FEB-2004; 2004US-00782020.  
XX  
19-FEB-2004; 2004US-00782096.  
XX  
19-FEB-2004; 2004US-00782141.  
XX  
19-FEB-2004; 2004US-00782570.  
XX  
19-FEB-2004; 2004US-00783417.  
XX  
(ATHE-) ATHENIX CORP.  
XX  
Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;  
WPI; 2004-635574/61.  
XX  
N-PSDB; ADR89400, ADR89401.

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Db 448 QLODSENELPETTGQPNYESYSHRLSHIGLISASHVKALVYSWTHSADRTNTINSDSI 507
Qy 515 TQIPAVKSYLYONLANAYTVIKGT-HTGGDLIRFLRTKSEYNNAVAGGIRLIINKKT 573
Db 508 TQIPLVKAFNLPSGAS-----VVRGPGFTGGDILQRTNTGT-----FGDIRVNIINPPF 555
Qy 574 AGQSYRIRFRYAADKAFFSVLYPGGWSNRFSVLEKSYSGNY-----DGLKYDFK 626
Db 556 A-QRYRIRIYASTNLEFHTSI--NGKAINQ-----GNFSATMNRGDDLDYKAFR 603
Qy 627 FAETITPLPSSNQMDVEMQANSFQSDVNVVLDKIEFLPSNTTTLLEYEGERDLEKTKNA 686
Db 604 TVG-FTTFFSFSAQSTFTIGANNFSLGNEVYIDRIEFVPEVT---YEAYDLKKAQDE 659
Qy 687 VNDLFTN 693
Db 660 ITAMFTS 666

```

## RESULT 12

```

ID CRIBA_BACTK STANDARD; PRT; 1228 AA.
AC POA373; P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Pesticidal crystal protein cryIaB (insecticidal delta-endotoxin
DE CryIaB(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIaB; Synonym=cryIA4, cryIaB(a);
OS Bacillus thuringiensis subsp. kurstaki.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=29339;
RN [1]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis.";
RL Nucleic Acids Res. 16:2723-2723(1988).
CC -I- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -I- SIMILARITY: Belongs to the delta endotoxin family.

```

```

CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----

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```

DR EMBL; X06711; CAA29898.1; -; Genomic_DNA.
DR PIR; S00873;
DR HSSP; P07130; IDLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1228 AA; 139648 MW; C8E3A19F5D98575 CRC64;

```

```

Query Match 19.3%; Score 705.5; DB 1; Length 1228;
Best Local Similarity 31.3%; Pred. No. 4.8e-40;
Matches 224; Conservative 118; Mismatches 279; Indels 95; Gaps 31;

```

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Qy 10 KNEVEILLESSNNTNTPNRYPPANNRDMSTMNDCCGISWDEIWSVEVITISGINLIE 69
Db 6 KNEEILINAVNSHSAQMDLLPDARIEDSLCIA-----EGNNIDP-FVSASTVQT-GINIAG 59
Qy 70 FVI-----EPSLGGINTLLS-IIGKLIPTNRQTVSALSICDLLSIIRKEVADSVLSDAIAD 124
Db 60 RIILGVLPAGQALSAFYSFLVGLWPRGRDQWE-IFLEHVEQLINQOITENARNTALAR 118
Qy 125 FDGKLNRYEYLYSILGAMLKDGKPKLOKTNNSDIGOLVY--YFKLSERDFNEILGSLSR 182
Db 119 LQGLGDSFRAYQOS-LEDW-----LENRDDARTSRVLYTQYIAL-ELDFLNAMPLFAIR 170
Qy 183 NNAQVLLLTFFAACAAVQVLLLRDAVQYKAQWPFPLSAENVRSSELISPSNGCFTGYYE 242
Db 171 NQ-EVPLLMVYAQAANLHLLLRDASLFGSE-FGLTSQEIQR-----YYE 213
Qy 243 RLKCKTAETNYCLYVYQVGLNOIKQGGTADTWSKFNKPRRMTLAVLDIIAIFPTYDF 302
Db 214 RQVERTRDYSDYCVENYNTGLNSLR--GTNAASWVYVYVQRRDLTGLVLDLVALFPSYDT 271
Qy 303 EKYPLPHTVELTREIYTDVAV--GYSSGTYSMLRNMPNTFNGLEANGTRGPGVLVTWLSKI 359
Db 272 RTYPINTSAQLTREYVYTDAGATGVNMAWNNWNNNAPSFAIEAASAIRSPHLLDFLEQL 331
Qy 360 GIYNEVYSRYFAGWGTGRHYEDYTKGNGIFORMSG-----TTSNDLRNIDPQNA 408
Db 332 TIFSA-----SSRWSNTRHM-TYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPASR 385
Qy 409 DVYKITSILAMLVGTTARTARPEVRSKADPRRVGGPDLNVAG-----NNGLSRMT 459
Db 386 DYTRESYAGVLLWG-IYLEPIHGVTVPFNFNPQNIS-DRGTANYSQYSPGGLQKLD 443
Qy 460 IESTF-PLVLHNGVRGSPHRLSNAACVYVYGVNSRVVYGTWHTSLKRENIIEANQITQIP 518
Db 444 SETLEPPETTERPNYESYSHRLSHIGIILQSRVNVVPVYSWTHRSADRTNTIGPNRITQIP 503
Qy 519 AVKSYVLYONLANAYTVIKGT-HTGGDLIRFLRTKSEYNNAVAGGIRLIINKTAGQS 577
Db 504 MVKASELPQ-----GTVVVRGPGFTGGDILR--RTNTG-----GFGPIRVTVNGPLT-QR 550
Qy 578 YRIRFRYAADKAFFSVLYPGGWSNRFSVLEKSYSGNYVDLYKSDKFAEIIITPPLPS 637
Db 551 YRIGFRYAS--TVDFDFVSRGTTVNNRFRFLRTNWSG--DELYGNF-VRRFTTPTFTF 605
Qy 638 SNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTTLLEYEGERDLEKTKNAVNDLFTN 693
Db 606 TQIQDIIRTSIQGLSGNGEVYIDKIEIP---VTATFEAYDLEAQAQAVNALFTN 658

```

## RESULT 13

```

Q93NM5 BACTU PRELIMINARY; PRT; 1228 AA.
ID Q93NM5;
AC Q93NM5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CryIaB.
GN Name=cryIaB;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Zhang J., Song F., Huang D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368257; AAK63251.1; -; Genomic_DNA.
DR HSSP; P07130; IDLC.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005107; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.

```

```
DR Pfam: PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1144 AA; 128060 MW; 98F93070C49014AB CRC64;

Query Match
Best Local Similarity 19.4%; Score 709; DB 2; Length 1144;
Matches 234; Conservative 123; Mismatches 266; Indels 126; Gaps 35;

QY 4 MSPYQNKNEYELLESSNNNTNPN--RYPFANNR--DMSTMSWDCQGISW---DEINES 56
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 59
QY 57 VETITS-----IGINLIEFV----BPSLGGINTLLS-IIGKLPTNRQTVALSICDILL 106
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 109
QY 60 PETFISSVTQIGIVGVGALGVPPAGQIASFYFVIGQLWPSSTVSVMEMKQVE 119
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 122
QY 107 SIIRKEVADVSLDAITPDGKLNRYEYLYSVLGAWLKDGKPLQKTNNSDI---GQLVY 163
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 166
QY 120 DLIDQKITDSVRKALAGLQG--LGDGLDYYQKSLKNWLE-----NRNDTRARSVVVT 170
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 173
QY 164 YFKLSRDFNEILGSSLSRNNAQVLLPTFAQANVQLLLLRDVAQYKAQWPFPLSAENV 223
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 226
QY 171 QXIALELDFVAKI--PSFALSGQEVPLLSVYAQAANLHLLLRDASIFGAEW--GFTPG-- 226
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 229
QY 224 RSELISPNSGCDFGTGDYERLACKTAETNYCLYVYQVGLNQIKOGGTGADTWSKFNKPR 283
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 286
QY 227 -----ISTFYDQVTRTAQYSDYCVKWNVTGLDKL--GTNAASWLKXHQPR 271
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 274
QY 284 REMTLAVLDIIAIFPYDEKPLPPLTHVELTREIYTDVAGY---SSGTY--SWLRNWPNT 338
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 341
QY 272 REMTLVLVDLVALFNNYDRTPIETTAQLTREVTDPVFNRETSGGFCRRWSLNSDTS 331
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 334
QY 339 ENGLEANGVRGCLVTLWSKIGLYNEVY-----SRYPAGWVGRHYEDYTKGNGIFQRM 392
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 395
QY 332 FSEVESAVIRSHPLFDLSEIEFYTRAGLPLNNTLEYVWGHISIKYKNTNASSALEKN 391
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 394
QY 393 SGT--TSNDLRNIDFQNAVYKITSLA--IMNLVGETTARPEYRVSKADPRRVGGPDLYND 449
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 452
QY 392 YGTITSNKIKYVDLANKDIFQVRSGLADLANIYAQV-----YGVVPYASFTLL--DKNTG 443
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 446
QY 450 AGN--NGLSRMTIESTPPLVLHNGV-----RQPSHRLS-----NAACVV 487
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 490
QY 444 SGSVGFTYSKPHITMQVCTQNYNTTIDEIPPEPLSGYSHRLSHITTSYSPSKNASSPA 503
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 506
QY 488 -YGNRVNVYVGHSTSLKRENIIEANQITQIPAVKSYQLONYLANAYTVVIKGT--HTGSD 545
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 548
QY 504 RYGN--LPFAMTHRSADVNTVYSDKITQIPVKAHTLV-----SGTTVIKPGPGFTGN 556
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 559
QY 546 LIRFLRTKS---EYNAVYAGGGIRLIINNKTAGQSYRIRFRYAADKAAPFVLYPGGWG 602
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 605
QY 557 ILK--RTSSGLAYTSVSV-----KSPLSQRYARIRYASTTNLRLFTI-----S 600
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 603
QY 603 SNRFVLSKYSQNY--DDLKYSDFKFAEIIITPPLSSNIQMDVEMQANSFQSDVNVLDK 661
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 664
QY 601 GTRIYSINVNTKMNKGDDLTFTNFDLATIGT--AFTFSNYSDSLTVGADSFASGGEVYDK 659
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 662
QY 662 IEPLSPNTTLEYEGERDLKTKNAVNDL 690
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 693
QY 660 FELIPVNAI---FEAEEDLDVAKKAVKNL 685
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 688

RESULT 11
CR1ID BACTU
ID CR1ID BACTU STANDARD; PRT; 719 AA.
AC Q9XDL1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Peptidicidal crystal protein cryl(d) (Insecticidal delta-endotoxin
DE CryII(d) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name-cryII; Synonyms=cryII(d), NrcryV;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
```

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Qy 386 NGIFORMSGTNSDLNIDFONADVYKI-----TSIAIMNLVGETTAR 428
Db 386 SS-FNKYSGLVAGAEIDIPVQNDIYRVVWTYIGRYNSLLGVNPNVTFYFSNNTQKTYSK 444
Qy 429 PEY---RVSKADFRVGGPDL---NYDAGNGLSRMT---IESTFPLVLHNSGVGRGSHR 479
Db 445 PKFAGGIKTID---SGEELTYENQSYSHRVSITYTSFEIKSTGGTVL---GV----- 491
Qy 480 LSNAACVVYGNRNVVYGTHTSLKRENIIEANOITQIPAVKSYLQNYLANAYTVYIKG 539
Db 492 -----VPIFGWTHSSASRNNFIYATKISQIPINKA---SRTSGGAVNPFQEG 535
Qy 540 THTGGDLIRLRTKSEYNNAVAGG-----IRLIINNKTAGOSYRIRFRYAADKAAPFSV 594
Db 536 LYNGGPMVKL-----SGSGSQVINLRVATDAKGASQRYRIRIRYASDRAGKFTI 584
Qy 595 YLPGGWSNRFVSLEKSYSGNY-----DDLKYSDFKFAIITPPPLSSNIQMDVE 645
Db 585 -----SSRSPENPATYSASIAYTNTMSTNASLTYSTPAYAE-----SGPINLGIS 629
Qy 646 MQANSFQSDV-----NVVLDKIEFLPSNTTILEYEGERDLEKTKUAVNDLFTN 693
Db 630 GSSRTFDISITKEAGANLYIDRIEFIPVNTL---FEAEDLDVAKAVNGLEFTN 681

```

## RESULT 9

```

Q6R2R6_BACTU
ID Q6R2R6_BACTU PRELIMINARY; PRT; 1160 AA.
AC Q6R2R6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE HBF-1 CryIII delta-endotoxin.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Song F., Zhu C., Zhang J.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY518201; AAR98783.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF03945; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1160 AA; 130452 MW; C794F99AD1397188 CRC64;

```

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Query Match 19.9%; Score 728.5; DB 2; Length 1160;
Best Local Similarity 29.9%; Pred. No. 1.1e-41;
Matches 232; Conservative 124; Mismatches 240; Indels 179; Gaps 34;

Qy 4 MSPYQNKNEYEILSSNNNTNPN---RYPFANNRDMSTWNSDCQGISWDE----- 52
Db 1 MSP-NKNEYEILDALSPTSVSDNSIRYPLANDQTTWLNQMYKYDKTKTESTNABLSRN 59

Qy 53 --TWSEVETITSIGINLIEFVIE---PSLGGINTLL-SIIGKLIPTNRQTYSALSICDL 105
Db 60 PGTFISQAQAVGTGDIVSTIISGLGIPVLGEVFSILGSLIGLLWPSNNENWQIFMNRV 119

Qy 106 LSIIRKEVADSVLSDAIAFDGKLNRYR---EYILSYLGAWLKDGKPLQKTNNSIGQVLV 162
Db 120 EELIDQKILDSVRSRAIAD-----LANSRIAVEYQNALEDWRKNP---HSTRSAAL---- 168

Qy 163 YYPKLSERDFN--EILG---GSLSRNNAOVLLLPTEFAQAAVOLLRLDRVAVQKQWFFP 217

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Db 169 -----VKERFGNAEAILRTNMGSPSQNTYETPLPTTAAQAASLHLVNRDVQIYKKEWG-- 222
Qy 218 LSAENVRSELISPSNOCDFGTGYERLCKKTABEYTNCLYVYQVGLNQIKQGGTGADTWS 277
Db 223 -----YQNDIDL---PYKEQVSYTARYSDHCQVQYNAGLNKLR--GTGAQKW 266
Qy 278 KFNKPREMTLAVLDIAIAPFTYDFPKYPLPHTVELTREIYTDVAG--YSSGTVSWLRNP 336
Db 267 DYNRRFRNMVWLDLVALFPNDYDARIYPLETNAELTREIFTDPVGSYVTVGQSSTLSIWY 326
Qy 337 N-----TFNGLEANGTRGPGLVTWLSKIGIYNEY-----VSRVFAGWCVTRHYEDVTGK 385
Db 327 DMIPALPFSFTLE-NLLAKPDPFTLLQIRMYTSFRONGTIEYVYWGQORLTLSIYG 385
Qy 386 NGIFORMSGTNSDLNIDFONADVYKI-----TSIAIMNLVGETTAR 428
Db 386 SS-FNKYSGLVAGAEIDIPVQNDIYRVVWTYIGRYNSLLGVNPNVTFYFSNNTQKTYSK 444
Qy 429 PEY---RVSKADFRVGGPDL---NYDAGNGLSRMT---IESTFPLVLHNSGVGRGSHR 479
Db 445 PKFAGGIKTID---SGEELTYENQSYSHRVSITYTSFEIKSTGGTVL---GV----- 491
Qy 480 LSNAACVVYGNRNVVYGTHTSLKRENIIEANOITQIPAVKSYLQNYLANAYTVYIKG 539
Db 492 -----VPIFGWTHSSASRNNFIYATKISQIPINKA---SRTSGGAVNPFQEG 535
Qy 540 THTGGDLIRLRTKSEYNNAVAGG-----IRLIINNKTAGOSYRIRFRYAADKAAPFSV 594
Db 536 LYNGGPMVKL-----SGSGSQVINLRVATDAKGASQRYRIRIRYASDRAGKFTI 584
Qy 595 YLPGGWSNRFVSLEKSYSGNY-----DDLKYSDFKFAIITPPPLSSNIQMDVE 645
Db 585 -----SSRSPENPATYSASIAYTNTMSTNASLTYSTPAYAE-----SGPINLGIS 629
Qy 646 MQANSFQSDV-----NVVLDKIEFLPSNTTILEYEGERDLEKTKUAVNDLFTN 693
Db 630 GSSRTFDISITKEAGANLYIDRIEFIPVNTL---FEAEDLDVAKAVNGLEFTN 681

RESULT 10
Q8KZL7_BACTG
ID Q8KZL7_BACTG PRELIMINARY; PRT; 1144 AA.
AC Q8KZL7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Cry8 protein.
GN Name=Cry8;
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OX NCBI_TaxID=29338;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SDS-502;
RA Asano S., Yamashita C., Iizuka T., Takeuchi K., Yamanaka S., Cerf D.,
RA Yamamoto T.;
RT "A strain of Bacillus thuringiensis subsp. galleriae containing a
RT novel cry8 gene highly toxic to Anomala cuprea (Coleoptera:
RT Scarabaeidae).";
RL Biol. Control 28:191-196(2003).
DR EMBL; AB089299; BAC07226.1; -; Genomic_DNA.
DR HSSP; Q06117; 1J16.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.

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Db      1  MNSYENKNEVEILLNDKSKNSMNPYLYRPLANDSLASMQNTNYKD-----WLTMCDDTDT 55
Qy      60  --ITSIGINLIEVIEPSLGGINTLLSIIGKLIPTNRQTVSAL-----
Db      56  DVLSSRG-----AVSTGVGLSTILSLFSG--IPLIGEGIDILLGAADFLWPESDGHQY 107
Qy     101  STCDLLSIIRKEVADSVL-----SDAIDFDGKLKNRYEYLSYLGAWLKD--GKPLQKTN 154
Db     108  TWEDLNWHT--EELMDERLETEKRTALDRLG--LKALLGLFDPADFSWEKQNDPLAKNR 165
Qy     155  NSDIGOLVYVYKLSERDFNEILGGLSRNNAQVLLPTFAQANVQLLLRDVAQYKQW 214
Db     166  ---VGG---YFEDVHTHFVKDMASIFSATNYEVLPLPVYAQAANLHLLLRREGVLYGSRW 219
Qy     215  FFLSNAENRSELISNSCDDTGDYERLCKTAYTYNYCLYVQVGLNQIKQGGTAD 274
Db     220  G-----IAP---AADF---YHDQLLYTAIYANHCVTYWYNNGLAQOQKELFAKSP 262
Qy     275  TWSKFKFRREMTLAVLDIIAIPPTDYFEKYPLPHTVELTRLEYTDVAGYSSGTYSWLNR 334
Db     263  NNRNFNAYRDMTITVLDIIALFPPTDYDARLYKPKTELTRLEYSDVNLND--VTGVQO- 319
Qy     335  WPNFNGLEANGTRGPGVLTWLSKIGIYNEYYSRYFAGVWGRHYEDYTKGNGIFQMS- 393
Db     320  --TDLNKNEAFTSRPHLVRLRGDFDYTRTKYAYWRYLAGHTNYFSFT--GNGTIYSSSF 376
Qy     394  -----GITSNDLRNIDFQNAVYKITSIAIMLVGETTARPEYRVSKADPRVGGDPLN 447
Db     377  NNMYDTMTKSTINIPDY--ANIYKLTWTSYTNISPYT---DPVGISQMFSLTNQOULT 431
Qy     448  YDAGNNGLSRMTIESTF-----PLVLHNGVRGSPHRLS--NAACVVYGNRVN-VY 496
Db     432  YT--GTSAPKYPVRETFEIPPTDEKPLYENY-----SHLSYMTSAQHFGDKKIGYTF 484
Qy     497  GHTWTSKRENTIEANQITQIPAVKSYLLQNYLANAYTVYIKGT--HTGGDLIRFLRTKSE 555
Db     485  AWWHESVDPNRVDPKITQIPAVKGDYDQ-----YGVYKQPGHGTGDLVSMIRTD-- 536
Qy     556  YNAVAGGIRLIIN-NKTAGOSYRIRFYADKAAFFSVLYPGWGNRFRVLSKSY- 613
Db     537  -----RGINYVFPQPLDYRIRIRYSTSNGY--LYTYS---PNTKIVILPPTTL 581
Qy     614  ---SGNYDDLYKSDPKFABIITPPLSSNIQMDVEMQANSFQSDV-----NV 657
Db     582  VDGQPTFDPMDSAFRVZV-----PA-----SFRASVAGYNTFTIEAGFGPV 624
Qy     658  VLDKIFLPSNTTTLTEYEGERDLEKTKNAVNDLFTN 693
Db     625  YIDKIEFIPDNTTTLTEYEGGRDLEKTKNAVNDLFTN 660

```

## RESULT 8

```

CR8CA_BACTP STANDARD; PRT; 1160 AA.
ID CR8CA_BACTP
AC Q45706;
DT 30-MAY-2000 (rel. 39, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DT 13-SEP-2005 (rel. 48, Last annotation update)
DE Pesticidal crystal protein cry8Ca (insecticidal delta-endotoxin
DE CryVIIIc(a) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein).
GN Name=cry8Ca; Synonyms=cryIII, cryVIIIc(a);
OS Bacillus thuringiensis subsp. japonensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=128936;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Buibui.
RX MEDLINE=94100786; PubMed=7764305;
RA Sato R., Takeuchi K., Ogiwara K., Minami M., Kaji Y., Suzuki N.,
RA Hori H., Asano S., Ohba M., Iwahana H.;

```

```

RT "Cloning, heterologous expression, and localization of a novel crystal
RT protein gene from Bacillus thuringiensis serovar japonensis strain
RT buibui toxic to scarabaeid insects.",
RL Curr. Microbiol. 28:15-19(1994).
RN [2]
RP PROTEIN SEQUENCE OF 1-14 AND 56-64, AND CHARACTERIZATION.
RX MEDLINE=94259659; PubMed=8200856;
RA Hori H., Suzuki N., Ogiwara K., Himejima M., Indrasith L.S.,
RA Minami M., Asano S., Sato R., Ohba M., Iwahana H.;
RT "Characterization of larvicidal toxin protein from Bacillus
RT thuringiensis serovar japonensis strain Buibui specific for scarabaeid
RT beetles.",
RL J. Appl. Bacteriol. 76:307-313(1994).
CC -!- FUNCTION: Promotes colloidsmetic lysis by binding to the midgut
CC epithelial cells of insects. Active on various scarabaeid beetles
CC such as Anomala cuprea, A. rufocuprea and Popillia japonica.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U04366; AAA21119.1; -; Genomic_DNA.
DR PIR; I40589; I40589.
DR HSP; Q06117; IJ16.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005639; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin M; 1.
DR Pfam; PF03945; Endotoxin N; 1.
KW Direct protein sequencing; Sporulation; Toxin.
SQ SEQUENCE 1160 AA; 130426 MW; C16C3D912BEB751 CRC64;

```

## Query Match

19.9%; Score 728.5; DB 1; Length 1160;

Best Local Similarity 29.9%; Pred. No. 1.e-41;

Matches 232; Conservative 124; Mismatches 240; Indels 179; Gaps 34;

Qy 4 MSPQNKNEYELSSSNNNTNPN--RYPFANNRDMSTMWDCQGISWDE----- 52

Db 1 MSP--NNQNEYEIIIDALSPTSVDNSIRYPLANDQNTLQNNMYKDYLKWTSTNAELSRN 59

Qy 53 --IWESVETITISIGINLIEFVIE---PSLGGINTLL--SIIGKLIPTNRQTVSALSICDL 105

Db 60 PGTISAQDVGTDGIDIVSTIIISGLGIPVLGEVSIILGSLIGLWPSNENVMQIFMNRV 119

Qy 106 LSIIRKEVADSVLSDAIDFDGKLKNRY--EYLSYLGAWLKDQKPLQKTNNSDQGLV 162

Db 120 EELIDQKILDSVRSRAID----LANSRIAYEYQNALEDWRKNP---HSTRSAAL----- 168

Qy 163 YFFKLSERDFN--EILG---GSLSRNNAQVLLPTFAQANVQLLLRDVAQYKQWPPF 217

Db 169 ---VKERFGNAEAILRNTMGSPQNTYETPLPTYAQAASLHLLVMRDVQIYKGEW- 222

Qy 218 LSAENRSELISPNSGCDFTGDYVYERLCKTAYNTYCLYVQVGLNQIKQGGTADTWS 277

Db 223 -----YPQNDIDL----FYKQSVSYTARSDHCVQYNAGLNKLR--GTAKQKWV 266

Qy 278 KFNKFRREMTLAVLDIIAIPPTDYFEKYPLPHTVELTRLEYTDVAG-YSSGTYSWLNRWP 336

Db 267 DYNRFRRENMVLDLVALFENYDARIYPLETNAELTREIFDTPVGSVVTGSSLTISWY 326

Qy 337 N-----TFNGLEANGTRGPGVLTWLSKIGIYNEY-----VSRYPAGVWGRHYEDYTKG 385

Db 327 DMIPALPSPFSTLE-NLLRKDPFTLLQEIIRMYTSFRQNGTIEYNNYWGQORLTLSIYTG 385



Db 392 PITNIRDNDIYKVDLRAAYVATIRNALDST-----FGVSSSHFFNNMGKNELYQS-KQPY 445  
 QY 456 SRMTTESTPLVLHNSG-VRGPSHLSNAACV-----VYGNRVVNYGTHTSLKRE 506  
 Db 446 PYPITITPGESLEGNVDYSHLLCNVKNITGGLRQTSARGRSLLSHAWTHKSLNPK 505  
 QY 507 NIEANQITQIPAVKSYLYQLANAYTYVIKGT-HTGGDLIRFLRTKSEYNAVYAGGI 565  
 Db 506 NIIAADKITHIPAVKSNL-----SASSAVIKPGFTGGDLR-LGPNOFVDYI----- 553  
 QY 566 RLIIINKTAGQSY-RIRFRYADKAFFSVLYPGGWSNRVSLK-KSYSGNYDDLKYS 623  
 Db 554 -LTPDNPQVSQIYDFVRLRYACMGGANILIQF-----WNKNWIGVQLVSTTSLENLKYE 608  
 QY 624 DKFAEIIIPPLSSNIQMDVMOANSFOSDVNVLDKIEFLPSTNTTLEYEGERDLEKT 683  
 Db 609 NFAY-----ITRLSFTFGQGGYNNISYNTSPNPNVLDKIEFLPVSQTPPEYEGKHLKNT 665  
 QY 684 KNVNDLFTN 693  
 Db 666 QADVNNLFLN 675

## RESULT 5

CR9AA\_BACTG  
 ID CR9AA\_BACTG STANDARD; PRT; 1156 AA.  
 AC Q9031; Q03747;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Pestidical crystal protein cry9Aa precursor (insecticidal delta-endotoxin CryIXA(a)) (Crystalline entomocidal protoxin) (130 kDa crystal protein)  
 DE Name=cry9Aa; Synonyms=cryIG, cryIVA(a);  
 OS Bacillus thuringiensis subsp. galleriae.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=29338;  
 RN [1] NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 24-34.  
 RP STRAIN=11-67;  
 RC MEDLINE=92070568; PubMed=1660003; DOI=10.1016/0014-5793(91)81144-W;  
 RX Smulevitch S.V., Osterman A.L., Shevelev A.B., Kaluger S.V.,  
 RA Karsan A.I., Kadyrov R.M., Zagnitko O.P., Chestukhina G.G.,  
 RA Stepanov V.M.;  
 RT "Nucleotide sequence of a novel delta-endotoxin gene cryIG of Bacillus thuringiensis subsp. galleriae.";  
 RL FEBS Lett. 293:25-28(1991).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE OF 1-1151.  
 RC STRAIN=DSIR517;  
 RX MEDLINE=92211329; PubMed=1556556;  
 RA Gleave A.P., Hedges R.J., Broadwell A.H.;  
 RT "Identification of an insecticidal crystal protein from Bacillus thuringiensis DSIR517 with significant sequence differences from previously described toxins.";  
 RL J. Gen. Microbiol. 138:55-62(1992).  
 CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut epithelial cells of insects. This protein is toxic to Galleria mellonella.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

DR EMBL; X58120; CAA41122.1; -; Genomic DNA.  
 DR EMBL; X58534; CAA41425.1; -; Genomic DNA.  
 DR PIR; S19306; S19306.  
 DR HSP; P02965; ICY.  
 DR InterPro; IPR003305; Cenc carb bd.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; Endotoxin C.  
 DR InterPro; IPR005639; Endotoxin N.  
 DR Pfam; PF02018; CBM\_4\_9; 1.  
 DR Pfam; PF03944; Endotoxin C; 1.  
 DR Pfam; PF00555; Endotoxin M; 1.  
 DR Pfam; PF03945; Endotoxin N; 1.  
 KW Direct protein sequencing; Sporulation; Toxin.  
 FT PROPEP 24 23 Removed in mature form.  
 FT CHAIN 24 1156 Pestidical crystal protein cry9Aa.  
 SQ SEQUENCE 1156 AA; 129727 MW; 785F65B1B1165FF2 CRC64;  
 Query Match 20.4%; Score 747; DB 1; Length 1156;  
 Best Local Similarity 30.6%; Pred. No. 5.7e-43;  
 Matches 230; Conservative 130; Mismatches 249; Indels 142; Gaps 31;  
 QY 9 NKNEYEILLESSNNNTNPN--RYPPANNRDMSTWMDCCQ---ISW-DEIWESEVETITS 62  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 QY 2 NONKHGIICAGSCGASDDVAKYPLANNPYSSALNLSCONSSILNWINIIGDAAKEAVS 61  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 QY 63 IGINLIEFVIEPSLGG-INTLLSIIIGKLI-PTNQTVSALSTCDLLSIIIRKEVADSVLSD 120  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 Db 62 IGTIVSLITAPSLTGLISIVYDLIGLVGGSSGOSISDLSTCDLLSIIIRVOSVSLD 121  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 QY 121 AIADFDGKLNKRYEYLYSLGAWLKGKPLQKTNNSDYGQVYVFKLSERDFNEIL---- 176  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 Db 122 GIAFNGSVLYRN-YLEALDSWKN-----PNSASAEELTRPRIADSEFDRLTRGS 174  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 QY 177 ---GGSLSRNAQVLLPTFAQAAVOLLRLDRAVQYKAQW-----PFPLSAENVRELI 228  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 Db 175 LTNGGSLARQNAQIILLPSFASAAFFHLLLRDATRYGTNNGLYNATPFINYQSKLVELI 234  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 QY 229 SPNSGCDFTGDYERLCKTAETNYCLYQVGLNQIKQGTGADTWSKKNKREMTL 288  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 Db 235 E-----LYTDYCVHWNGFNELRQGTSAATWLEFHYRREMTL 274  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 QY 289 AVLDIILFPTDYFEKYPPLTHVELTRIYTDVAGY-----SSGTYSMWR--NWPNTFNGL 342  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 Db 275 MVLIDIVASFSLDITNPIEDTQFLSRVIYTDPIGFVHRSSLRGESWFSFNRRAN-FSDL 333  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 QY 343 EANGTRGPGLVTWLSKIGIYNEYSVRYPAG-----WVGRHYEDYTKGNGIFORMSGT 395  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 Db 334 E-NAIPNPRPSWFLNNMIISTGSLTLPVSPSTDRARVWYSGRDRISPANSQFTELISQ 392  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 QY 396 TSNDLRNIDFONADVYKITSIAIMNLVGETTARPEYRYSKADPRVGGPDLYDAGNGL 455  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 Db 393 HTTATQTILGRN--IFRVDSQA-CNL-NDTT-----YGVNRAVF-----YHDASEGS 435  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 QY 456 SRMTIESTFPLVLHNSGVGRP-----SHRLSNAACVVVG-----489  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 Db 436 QRSYVEG-----YIRTGIDNPRVQINITYLPGENSIDTPEDYTHILSTINLTCGLRQV 491  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 QY 490 ----NSRVNVYGVTHTSLKRENIIEANQITQIPAVKSYLYQLANAYTYVIKGTHTCGD 545  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 Db 492 ASNRSSSLVMYGVTHKSLARNNTINPDRIQTPLTK-----VDTRGTGVSYVNDPGFIGGA 547  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 QY 546 LIRFLRTKSEYNAVYAGGIGIRLIINNKTAGOSYRIRFRYADKAFFSVLYPGGWSNR 605  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 Db 548 LLQ-----RTDHGSL-----GVLRVQFPLHLRQOYRIRVRYASTTIRLSV-----NGS 591  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 QY 606 FVSLKSYSGNY---DOLKYSDFKFAEITTPPLP-SSNIQMDVEMQANSFOSDVNVVLDDK 661  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 Db 592 FGTISQNLPSMTWRLGEDLRYSFAIRENTSIRTASPDQIRLTIEPSFIRQEVYV--DR 649  
 QY 662 IEFILPSNTTILEYEGERDLEKTKNAVNDLFT 692  
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||  
 Db 650 IEFIPVNPTR--EAKEDLEAAKKAVALSFT 677

```
CC terminus.
CC -|- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U88188; AAC61891.1; -; Genomic DNA.
CC HSP; Q06117; J16.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Sporulation; Toxin.
CC NON TER 674
CC SEQUENCE 674 AA; 75959 MW; DA3904DAB891C978 CRC64;
CC
CC Query Match 22.7%; Score 831; DB 1; Length 674;
CC Best Local Similarity 31.9%; Pred. No. 3.8e-49;
CC Matches 236; Conservative 131; Mismatches 257; Indels 116; Gaps 31;
CC
CC QY 4 MSPYQNKNEYEILESSNNNTNPNYPFANN-----RDMSTMSW-NDCOG--ISWDEIWE 55
CC Db 1 MNQYQNKNEYEILESSNNNMNPNYPFADDPNAVMMKNGYKDWVNECEGNSVSPSAAA 60
CC
CC QY 56 SVETITSGINLIEFVIEPSLGGINTLLSIIGKLIPTNQTYSALSIDLLSIIIRKEVAD 115
CC Db 61 ITSQIVSVLTKLAKAVASSLA--DSIKSLGSLGSKITENNVSQVSNVQVHQLINRIQIE 118
CC
CC QY 116 SVLSDAIADPDGKLKNRYEYLSYLGAWLKDGKPLQKTNNSDIG---QLVYYPFKLSERDF 172
CC Db 119 TILDGESSLGLVAIYNRDYLGALEAW-----NNKNSINYQTNVAEAKTVEREF 170
CC
CC QY 173 NEILGSLSRNNAQVLLPTFAQAANVOLLRLDRDAVOYKAQWPFPLSAENVRSLSIPNS 232
CC Db 171 FTKLKIYRTSSQITLLPTFAQAANLHLSMLRDAVMYQEGW-----NLQSHI----- 218
CC
CC QY 233 GCDFTGDYERLCKTAETNYCLYWQVGLNQIKQGGTADTWKFNKFRREMTLAVLD 292
CC Db 219 -----NYSKELDDALEDYTNVCVEYTKGLNALR--GSTAID-WLEFNSFRDMLTMLDLVA 270
CC
CC QY 293 ILAIFPTYDEKPLPHVELTREIYTDVAGYSSGTYSLRNWPNP-----FNGLEANG 346
CC Db 271 LVAIFENYNVRYPLSTKISLRSKIYDTPVGRDTPS--FGDWTNTRTLANFENDLEREV 328
CC
CC QY 347 TRGPGLVTLWSKIGIYNEVYSRY-----FAGVGTGRHYEDYT-KNGIIFORMSGTT- 396
CC Db 329 TDSPLVKVLGDMTIYTGAIYSRPTSPGDRIGWYGNINAFYHTGRTDVMVFRQTGDTA 388
CC
CC QY 397 ----SNDLRNIDFQNAADVYK--ITSLAIMNLVG--ETTARPEYRVSKADPRRVGGPDLY 448
CC Db 389 YEDPSTFISILYD--DIYKLDRAAAVSTIQAMDIT---FGVSSSPFDIRGNQLY 442
CC
CC QY 449 DAGNNGLSRMTEISTPFLVLSNG-VRGPSHRL-----SNAACVYVYNSRVNVYGWTH 500
CC Db 443 QS-NKPYPSLPITITPGEESSEGNANDYSHLLCDVKILQEDSSNICEGRSSILSHAWTH 501
CC
CC QY 501 TSLKRNENIEMANOITQIPAVKSYLQNYLANAYTVYIKGT-HTGGDLIRPLRTKSYNAV 559
CC Db 502 ASLDRNTLIPDEITQIPAVTAYELR-----GNSSVAVGPGSTGGDLV-----KMSYHSV 551
CC
CC QY 560 YAGGGIRLIINNTAGQSYRIRRYAADAAPF-----SVVLYPGGWSNRFVLSKSY 613
CC Db 552 WS----FKVYCSSEL--KNTRVRIRYASHGNCQFLMKRWPNSTGVAPQWARH---NVQGTG 602
CC
CC QY 614 SGNYDDLKYSDFKFIABITPPLPSSNIQMDVENQANSFQSDVNVVLVDKIEFLPSNTTILE 673
CC Db 603 S---NSMRYEAPKYLDIFITPEENNFAFTIDLESG-----DLFDKIEFIPVSSAFE 654
```

```
QY 674 YGERDLEKTKQAVNDLFTN 693
Db 655 YEGKQNIETQKAVNDLFIN 674

RESULT 4
Q6BCH5 BACTU
ID Q6BCH5 BACTU PRELIMINARY; PRT; 675 AA.
AC Q6BCH5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Delta-endotoxin.
GN name=cry24-like;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=96-OK-85-24;
RA Ohgushi A., Saitoh H., Wasano N., Ohba M.;
RT "Cloning and characterization of novel cry genes from a mosquitoicidal
RT Bacillus thuringiensis serovar sotto strain";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB185105; BAD32657.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 675 AA; 75906 MW; E983D92F9053AEE8 CRC64;

Query Match 21.5%; Score 787; DB 2; Length 675;
Best Local Similarity 32.7%; Pred. No. 4.5e-46;
Matches 239; Conservative 109; Mismatches 286; Indels 96; Gaps 26;

QY 4 MSPYQNKNEYEILESSNNNTNPNYPFANN-----RDMSTMSW-NDCOG--ISWDEIWE 55
Db 2 VNPYQNKESVFEYHSHNNQKIDPNRYPTNPNNAVMMKNGYKDWVNECEGNSVSPSAAA 61
QY 56 SVETITSGINLIEFVIEPSLGGINTLLSIIGKLIPTNQTYSALSIDLLSIIIRKEVAD 115
Db 62 VTSALISIVLTKLAKALVSSL--VDAIKSSLSGISEVITKNNVSQLSMELVNQLINRIQIE 119
QY 116 SVLSDAIADPDGKLKNRYEYLSYLGAWLKDGKPLQKTNNSDIGQLVYYPFKLSERDFNEI 175
Db 120 TIMDLGASLNGLMGIYKR-YLNALNWDKD-----KSNITLQENVIEEFKYVESPFEN 173
QY 176 LGGSLSRNNAQVLLPTFAQAANVOLLRLDRDAVOYKAQWPFPLSAENVRSLSIPNSGCD 235
Db 174 LKGIYRTSSQITLLPTFAQAANLHLSMLRDAVMYQEGW-----NLQSHL----- 218
QY 236 FTGDIYERLCKTAETNYCLYWQVGLNQIKQGGTADTWKFNKFRREMTLAVLDITA 295
Db 219 ---DYKMELDIALKDYTNVCVEYVNRGLNALR--GSTALD-WLEFNSFRDMLTMLDLVA 273
QY 296 IPFTYDFEKYPLPHVELTREIYTDVAGYSSGTYSLRNWPNP-----FNGLEANGTRG 349
Db 274 IFPNYDVPQYPLTKIGLSRKIYDTPVGTTRTD--FGNWTLTDRLANFNDLERDVTDS 331
QY 350 PGLVTLWSKIGIYNEVYSRY-----FAGVGTGRHYEDYTKNGIIFORMSGTTSNDL 400
Db 332 PSLVKWLVDMMNIYTGAIYSPIGPGGERIGVYVGNMNSFVLTSRELSSYNYGEIAHED 391
QY 401 RNIDFQNAADVYKITSLA-----IMNLVGETTARPEYRVSKADPRRVGGPDLYDAGNGL 455
```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2005, 11:08:04 ; Search time 232 Seconds  
(without alignments)  
2107.462 Million cell updates/sec

Title: US-10-781-979-3  
Perfect score: 3655  
Sequence: 1 MKQMSFYQNKVEYIELSSS.....YEGERDLETKNAVNDLFTN 693

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues  
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2329.5	63.7	666	2	Q8VW62_BACTU
2	1745	47.7	666	2	Q7X3F7_BACTU
3	831	22.7	674	1	C24AA_BACTU
4	787	21.5	675	2	Q6BCH5_BACTU
5	747	20.4	1156	1	Q99031_BACTU
6	745	20.4	1169	1	CR8BA_BACTU
7	729	19.9	660	2	Q8RQU6_BACTU
8	728.5	19.9	1160	1	CR8CA_BACTU
9	728.5	19.9	1160	2	Q6R2R6_BACTU
10	709	19.4	1144	2	Q8KZL7_BACTU
11	707.5	19.4	719	1	CR1ID_BACTU
12	705.5	19.3	1228	1	CR1BA_BACTU
13	704.5	19.3	1228	1	Q93NM5_BACTU
14	702.5	19.2	1228	1	CR1BA_BACTE
15	702.5	19.2	1228	2	Q93T75_BACTE
16	690.5	18.9	675	1	C25AA_BACTU
17	689	18.9	849	2	Q6PYW8_BACTU
18	689	18.9	1227	1	CR1BE_BACTU
19	680	18.6	1215	1	CR1KA_BACTM
20	680	18.6	1231	2	Q8KNY2_BACTU
21	679	18.6	719	1	CR1IA_BACTK
22	679	18.6	719	2	Q6X181_BACTU
23	679	18.6	719	2	Q546K2_BACTK
24	679	18.6	719	2	Q581W9_BACTU
25	679	18.6	720	2	Q4LDH4_BACTU
26	679	18.6	746	2	Q4W4S8_BACTU
27	678.5	18.6	719	1	CR1IB_BACTE
28	678	18.5	719	2	Q93NJ5_BACTU
29	678	18.5	1229	1	CR1BC_BACTU
30	678	18.5	1233	1	CR1BD_BACTM
31	677	18.5	1231	1	CR1BD_BACTZ

32	676	18.5	719	2	Q8KY61_BACTU	Q8ky61 bacillus th
33	674.5	18.5	719	2	Q9FOP8_BACTU	Q9fop8 bacillus th
34	673	18.4	719	2	Q85796_BACTK	Q85796 bacillus th
35	672	18.4	1157	1	CR8AA_BACUK	Q45704 bacillus th
36	659	18.0	686	2	Q75QQ5_BACTE	Q75qq5 bacillus th
37	636.5	17.4	1163	2	Q5XLA8_BACTP	Q5xla8 bacillus th
38	636	17.4	659	1	CR3BA_BACTO	Q17699 bacillus th
39	631.5	17.3	852	2	Q643Z7_BACTU	Q643z7 bacillus th
40	631.5	17.3	852	2	Q9S6N9_BACTU	Q9s6n9 bacillus th
41	627.5	17.2	652	2	Q6PXN8_BACTU	Q6pxn8 bacillus th
42	624.5	17.1	644	1	CR3AA_BACTD	Q0a381 bacillus th
43	624.5	17.1	644	1	CR3AA_BACTM	Q0a380 bacillus th
44	624.5	17.1	644	1	CR3AA_BACTT	Q0a379 bacillus th
45	623.5	17.1	644	2	Q5EGP3_BACTT	Q5egp3 bacillus th

ALIGNMENTS

RESULT 1  
Q8VW62\_BACTA PRELIMINARY; PRT; 666 AA.  
AC Q8VW62;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Putative mosquitoicidal toxin (fragment).  
GN Name=cry40A;  
OS Bacillus thuringiensis (subsp. aizawai).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=1433;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Ito T., Sahara K., Amano S., Bando H.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB074414; BAB72018.1; -; Genomic\_DNA.  
DR HSSP; Q06117; 1J16.  
DR GO; GO:0008237; F:metallopeptidase activity; IEA.  
DR GO; GO:0005102; F:receptor binding; IEA.  
DR GO; GO:0006952; P:defense response; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR GO; GO:0030435; P:sporulation; IEA.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR000834; Peptidase\_M14.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
DR PROSITE; PS00133; CARBOXYPEPT\_ZN\_2; UNKNOWN\_1.  
FT NON\_TER  
SQ SEQUENCE 666 AA; 75311 MW; A87853FAE8FAM41D CRC64;

Query Match	63.7%;	Score	2329.5;	DB 2;	Length	666;			
Best Local Similarity	67.2%;	Pred. No.	1.2e-153;						
Matches	470;	Conservative	62;	Mismatches	116;	Indels	51;	Gaps	12;
QY	7	YONKNEYELSSSSNTNTPNRYFPANRDMSTMNDCCQISWDEIWESVETITSIGIN	66						
Db	3	YENKNEYELSSSSNTNTPNRYFPANRDMSTMNDCCQISWDEIWESVETITSIGIN	62						
QY	67	LIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDILLSIRKEVADSVLSDAIDP-	125						
Db	63	LIEFLMEPSLGGINTLFSIIGKLIPTNHQSVSALSICDILLSIRKEVADSVLSDAICRFL	122						
QY	126	DGKLNRYEYLYSYLGAWLKDGKPKQKTNNSDIGOLVYFKLSERDFNEILGGSLSRNA	185						
Db	123	DGKLNRYEYLYSYLGAWLKDGKPKQKTNNSDIGOLVYFKLSERDFNEILGGSLSRNA	182						
QY	186	QVLLPPTFAQANVQLLRDAVQYKAQWFPFLSAENVRSELISPNSGCDFGTGDYERLK	245						
Db	183	QILLPYPFCASCKCOLLRDAVQYEQWFPFLSAENVRSELISPNSGCDFGTGDYERLK	242						



C;Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Oct-2004  
C;Accession: I39811  
R;Donovan, W.P.; Rupa, M.J.; Slaney, A.C.; Malvar, T.; Gawron-Burke, M.C.; Johnson, T.B  
Appl. Environ. Microbiol. 58, 3921-3927, 1992  
A;Title: Characterization of two genes encoding Bacillus thuringiensis insecticidal crys  
A;Reference number: I39811; MUID:93119147; PMID:1476436  
A;Accession: I39811  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-652 <RES>  
A;Cross-references: UNIPROT:Q06117; UNIPARC:UPI0000126C14; GB:M89794; NID:g142729; PIDN:  
C;Genetics:  
A;Gene: cryIIIB2  
C;Superfamily: Parasporal crystal protein

Query Match 16.6%; Score 605; DB 2; Length 652;  
Best Local Similarity 27.6%; Pred. No. 4.7e-33;  
Matches 201; Conservative 141; Mismatches 241; Indels 146; Gaps 35;  
  
QY 4 MSPVQNKVEYELLESSNN--TNPTRYPFANNRD--MSTMWNCQGISWDEIWE--- 55  
DB 1 MNP-NKSEHDTIKVTPNSELOTN-HQYPLADNPSTLEELNYKGFRLMTEDSDSTEVL 58  
  
QY 56 --SVETITSGINLIEFVI---EPLSGGINTLL-SIIGKLIPTNRQTVSALSICDLLSI 108  
DB 59 NSIVKDAVGTGISVVGQILGVGVPPAGALTSFYQSFLNTIMFSDADPWKAP-MAQVEVL 117  
  
QY 109 IRKEVADSVLSDAIADPGKLNRYEYLSYGAWLKDGKPLQKTNNSDIGQLVYFVKLS 168  
DB 118 IDKIEYAKSKALAELOQ-LQNNFEDYNALNSWKTKPLSLRSKRSQD--RIREFSQA 174  
  
QY 169 ERDFNEILGSLSRNNAQVLLLPFAQAANVQLLLRDVAVQYKAQFPPLSAENVSELI 228  
DB 175 ESHFRNSM-PSFAVSKFEVLFLPYAQAANTHLLLDKAQVGEW--GYSSSDV----- 226  
  
QY 229 SPNSGCDFTGDYERLCKTAETNYCLYVYVGLNQIKQGGTGADTWKFNKFRREMTL 288  
DB 227 -----AEFVHRQLKLTQQYTHCVNWNVGLNGLR--GSTYDAWKFNFRREMTL 275  
  
QY 289 AVLDDIIAIPFYDFEYKPLPHTVELTREIYTDVAVGSSGTYSWLRNPNFTNGLEANGTR 348  
DB 276 TVLDDLVLFPFYDIRLYSKGKVELTRDIFTDPI-FSLNT---LQBYGPTFLSIE-NSIR 330  
  
QY 349 GPGLVTLWLSKIGIYNEVSRYPAGVGTGRHYEDYTKNGIFQMS-----GTT 396  
DB 331 KPLFDYLOGI-----BFHTRLQPGYFGKOSF-NYWSGNVYETRPSIGSSKTIITSPYGDK 385  
  
QY 397 SND-LRNIDFQNAADVYKITSALIMNLVGETTARPEYRVSKADFRYVGGPDNLNAGNGL 455  
DB 386 STEPVQKLSPDGQKYR--TIANTDVANWPNKGKYLGVTKVDFSQ-----YDDQKNET 436  
  
QY 456 SRMTIESTPPLVHNSG-----VRGPHRLSNAACVVYGNR--V 493  
DB 437 STQTYDSK-----RNNGHVSAQSDIDQLPETTDEPLEKAYSHOLNVAECFLMQDRGTI 491  
  
QY 494 NVYGTWHTSLKRENIIEANQITQIPAVKSYLQNYLANAYVIKGT-HTGGDLIRFLRT 552  
DB 492 PFTWTWRSYDFNTIDAELITQPLVYKAYALSSGAS-----IIEGPGFTGGNLL-FLKE 545  
  
QY 553 KSEYNVAVAGGGRLLIINNKTAGQSYRIRPRYAA-----DKAAFFSVLYPGWG 602  
DB 546 SENSIAKF-----KVTLNSALLQRYRVRIRYASTNLRFLVQNSNDFLVYI----- 594  
  
QY 603 SNRFVLSKSYSGNYDDLYSDFKFAEITTPPLPSSNI-----QMDVEMQANSQSDVNV 657  
DB 595 -NKTMKD-----DDLTYQTDLA-----TTNSNMGFSGDKNELIIGAESFVSENEKI 640  
  
QY 658 VLDKIEFLP 666  
DB 641 YIDKIEFIP 649

S39536  
Parasporal crystal protein cry9Ba1 - Bacillus thuringiensis  
N;Alternate names: delta-endotoxin-related protein; parasporal crystal protein cryX  
C;Species: Bacillus thuringiensis  
C;Date: 07-Oct-1994 #sequence\_revision 01-Dec-1995 #text\_change 05-Oct-2004  
C;Accession: S39536  
R;Shevelev, A.B.; Svarinsky, M.A.; Karasin, A.I.; Kogan, Y.N.; Chestukhina, G.G.; Stepa  
FEBS Lett. 336, 79-82, 1993  
A;Title: Primary structure of the cryX, the novel delta-endotoxin-related gene from Bac  
A;Reference number: S39536; MUID:94085596; PMID:8262221  
A;Accession: S39536  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1154 <SHE>  
A;Cross-references: UNIPROT:Q45745; UNIPARC:UPI00001781A3; EMBL:X75019  
C;Superfamily: Parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 16.5%; Score 603.5; DB 2; Length 1154;  
Best Local Similarity 28.4%; Pred. No. 1.3e-32;  
Matches 200; Conservative 107; Mismatches 253; Indels 143; Gaps 30;  
  
QY 56 SVETITSGINLIEFVIEP---SLGGINT--LLSIIGKLIPTNRQTVSALSICDLLSIIR 110  
DB 50 NVRTGLQTGIDIVAVVVGALGPGVGILTGFLSTLFGFLWPSNDQAWAEAFIQMEELIE 109  
  
QY 111 KEVADSVLSDAIADPGKLNRYEYLSYGAWLKDGKPLQKTNNSDIGQLVYFVKLSER 170  
DB 110 QRISDQVVRTALDGLTG-IQYNNQYLIALKEW-----EERPNGVRLANLVLRQFELIHA 162  
  
QY 171 DFNEIL---GGSLSRNNAQVLLLPFAQAANVQLLLRDVAVQYKAQFPPLSAENVSELI 227  
DB 163 LFWSSMPSPSGSGGQRFQALLVYVYQAANLHLLLDADAKEYGARW-----GURESQ 215  
  
QY 228 ISPNSGCDFTGDYERLCKTAETNYCLYVYVGLNQIKQGGTGADTWKFNKFRREMT 287  
DB 216 IG-----NLYFNELOTRTDYTHCVNWNVGLNGLR--GTSAESWLKHYHQFREAT 265  
  
QY 288 LAVLDIIAIPFYDFEYKPLPHTVELTREIYTDVAVGSSGTYS-----WLRNPNFT 338  
DB 266 LMADLIALFPYNTRRYPIAVNPQLTREYVTDPLGVPSSESLFPELRLRQWETSAMT 325  
  
QY 339 ENGLEANGTRGGLVTLWLSKIGIYN-----EYVSRYFAGVGTGRHYEDYTKG-----NG 387  
DB 326 FSNLENALISSPHLFDITNNLMYTGSPSVHVTNQLIEGWIG-----HSVTSSLLASGPTT 381  
  
QY 388 IFQMSGTTSDNLRNIDFQNAADVYKI-----TSLAIMNLVGETTARPEYRVSKADFRYV 442  
DB 382 VLRRNYGTTISVNYFSDNDRDYYQINTRSHTGLGFQN-----APLFGITPAQF----- 430  
  
QY 443 GPDLNVDAGNGLSR---MTIESTPPLV-----LHNSG--VRGPHRLSNAACVVY----- 488  
DB 431 -----YPGGYTSVTQRNALTCQNTYSIDELPSLPNEPISRSYSHRLSHITSYLHRVLT 485  
  
QY 489 -----CNSRVNVYGTWHTSLKRENIIEANQITQIPAVKSYLQNYLANAYVIKGT 540  
DB 486 IDGINYSGN--LPTVYVWTRDVTNLTITADRIITQLPLVKFEP-----AGTTVVVRGP 538  
  
QY 541 -HTGGDLIRFLRTKSEYNVAVAGGGRLLIINNKTAGQSYRIRPRYAAADKAFFSVLY----- 596  
DB 539 GFTGGDILR--RT-----GVGTFFGIR-VRTTAPLTQRYRIRFRPASTTNLFIGIRVGDR 590  
  
QY 597 -----YPGWGSNRFVLSKSYSGNYDDLYSDFKFAEITTPPLPSSNIQMDVEM-----QAN 649  
DB 591 QVNYFDFGRTMNR-----GDELRYESFATREFTT-----DFNFRQPQELISLVFAN 635  
  
QY 650 SFQSDVNVVLDKIEFLPSTNTTLEYEGERDLEKTKYNAVNDLFT 692  
DB 636 AFSAGQEVYFDRIRIIPVNPAP---EAKEDLEAAKKAVALSLFT 675

A:Title: Functional analysis of block 5, one of the highly conserved amino acid sequence  
A:Reference number: S48691; MUID:94307434; PMID:7913448  
A:Accession: S48691  
A:Molecule type: DNA  
A:Residues: 667-676 <NIS>  
A:CROSS-references: UNIPARC:UPI000017819A  
C:Superfamily: Parasporal crystal protein  
C:Keywords: delta-endotoxin

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Query Match      16.6%; Score 606.5; DB 2; Length 1180;
Best Local Similarity 28.7%; Pred. No. 8.7e-33;
Matches 223; Conservative 117; Mismatches 277; Indels 159; Gaps 42;

QY  4 MSPYQNKNEYETLASQKLNINNYTRYPIENSPKQLQSTNYKDWMLNMCQOQYGGD 49
DB  1 MNPYQNKNEYETLASQKLNINNYTRYPIENSPKQLQSTNYKDWMLNMCQOQYGGD 60
QY  50 WDEIWESVE---TITSGINLIEFVIEPSLG---GINTLLSIIIGKLIPTNRQTVS-AL 100
DB  61 PETFIDSGELSAITIV-VGTVLGTGFTPLGLALIGFTGLIPV---LFPADQSNWSD 116
QY  101 SICDLLSIIRKEVADSVLSDAIDFDGKLNRYEY-----YLSYLGAWLKDGKPKLOKTN 155
DB  117 FITQTKNIIKKEIASTYSNA-----NKILN-RSFNVISTYHNHLKTWENNPNP---QNT 167
QY  156 SDIG---OLVYFVKLSERDFNEI---LGGSLSRNN-----OVLLPPTFAQANVOLLLL 204
DB  168 QDVRTQIQLVHY-----HFQNVIPELVNSCPNPSDQDYNNILVLSVAQAANLHLTVL 221
QY  205 RDAVQYKAQWPFPLSAENVRSSELISPNSCDFTGDYERLCKTAETNYCLYVYQVGLN 264
DB  222 NQAVKFEA---YLK-NRQFDYLEP---LPTAIDYVPLTKAIEDYNYCVTYTKKGLN 273
QY  265 QIK-----QCGTGADTWKFNKFRREMTLAVLDIIAIFPTDYDEKPLPHVELTREIYTD 320
DB  274 LIKTPDSNLGDNINMNTYRTKMTTAVLDVALFPNDYDVGKYPGVQSELTEIY-Q 332
QY  321 AVGSSGTYSWLRNPNFTNGLEANGTRGPGVLTWLSKIGIYNE---YVSRYFAGWVGR 377
DB  333 VLNFESPKYKY-----DFQYQEDSLTRRPHLFTWLDLSLNFYEKAQTTPNPNF---TS 382
QY  378 HYE---DYTKGNGIIFORMSGTTSNDLRNIDFQNAVYKITSLA-----IMNLVG-ET 428
DB  383 HYNMFHYTLDN-ISQKSSVFGNHNV-----TDKLSGLATNIYIFILNVLSDNKYL 434
QY  429 PEY-RVSKADF-----RRVGGPDLYNADGN--GLSRMTIESTPPLVLSHNGV 473
DB  435 NDYNNISKMDFFITNGTRLEKELTAGSQITYDVNKNIFGL-----PILKRRENQ 485
QY  474 RGP-----SHRLS---NAACVYGNRVNVTGTHSLKRENIETANQITQIPAVK 521
DB  486 GNPTLFPYDNYSHILSFKLSIPATYKTQVTFATWTHSSVDPKNTIYTHLTQIPAVK 545
QY  522 SYLLQNYLANAYTVYIKGTHGTGDLIRFLRTKSEYNAVYAGGIRLIINNKTAGOSYRIR 581
DB  546 A-----NSLGTASKVQGPCHTGGDLIDF---KDHF-----KITQHSNFOQSYFIR 589
QY  582 FRYADKAAPFSVYL---YPGGWSGNRFVSLKESYSG-NYDDLKYSDPKFABIITPPLPS 637
DB  590 IRYASNGSANTRAVINLSIPG---VAELGMLNPTFSGTDYTNLKYDKQFYLEFSNEVKFA 647
QY  638 SNIQMDVEMQANSFOSDVNVVLDKIEFLPSNTTILEYEGEDRLEKTKAVNDLFTN 693
DB  648 PNQNISLVNRSVDVYNTNTVLIDKIEFLPITRSIREDEKQKLETVOQIINTFYAN 703
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## RESULT 13

I39870

parasporal crystal protein ISRH4 - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Oct-2004  
C:Accession: I39870  
R:Sen, K.; Honda, G.; Koyama, N.; Nishida, M.; Neki, A.; Sakai, H.; Himeno, M.; Komano,

Agric. Biol. Chem. 52, 873-878, 1988  
A:Title: Cloning and nucleotide sequences of the two 130 kDa insecticidal protein genes  
A:Reference number: I39869  
A:Accession: I39870  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1180 <RES>  
A:CROSS-references: UNIPROT:P16480; UNIPARC:UPI0000001B1F; GB:D00248; NID:G216289; PIDN  
C:Superfamily: Parasporal crystal protein  
C:Keywords: delta-endotoxin

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Query Match      16.6%; Score 605.5; DB 2; Length 1180;
Best Local Similarity 28.7%; Pred. No. 1e-32;
Matches 223; Conservative 117; Mismatches 277; Indels 159; Gaps 42;

QY  4 MSPYQNKNEYETLASQKLNINNYTRYPIENSPKQLQSTNYKDWMLNMCQOQYGGD 49
DB  1 MNPYQNKNEYETLASQKLNINNYTRYPIENSPKQLQSTNYKDWMLNMCQOQYGGD 60
QY  50 WDEIWESVE---TITSGINLIEFVIEPSLG---GINTLLSIIIGKLIPTNRQTVS-AL 100
DB  61 PETFIDSGELSAITIV-VGTVLGTGFTPLGLALIGFTGLIPV---LFPADQSNWSD 116
QY  101 SICDLLSIIRKEVADSVLSDAIDFDGKLNRYEY-----YLSYLGAWLKDGKPKLOKTN 155
DB  117 FITQTKNIIKKEIASTYSNA-----NKILN-RSFNVISTYHNHLKTWENNPNP---QNT 167
QY  156 SDIG---OLVYFVKLSERDFNEI---LGGSLSRNN-----OVLLPPTFAQANVOLLLL 204
DB  168 QDVRTQIQLVHY-----HFQNVIPELVNSCPNPSDQDYNNILVLSVAQAANLHLTVL 221
QY  205 RDAVQYKAQWPFPLSAENVRSSELISPNSCDFTGDYERLCKTAETNYCLYVYQVGLN 264
DB  222 NQAVKFEA---YLK-NRQFDYLEP---LPTAIDYVPLTKAIEDYNYCVTYTKKGLN 273
QY  265 QIK-----QCGTGADTWKFNKFRREMTLAVLDIIAIFPTDYDEKPLPHVELTREIYTD 320
DB  274 LIKTPDSNLGDNINMNTYRTKMTTAVLDVALFPNDYDVGKYPGVQSELTEIY-Q 332
QY  321 AVGSSGTYSWLRNPNFTNGLEANGTRGPGVLTWLSKIGIYNE---YVSRYFAGWVGR 377
DB  333 VLNFESPKYKY-----DFQYQEDSLTRRPHLFTWLDLSLNFYEKAQTTPNPNF---TS 382
QY  378 HYE---DYTKGNGIIFORMSGTTSNDLRNIDFQNAVYKITSLA-----IMNLVG-ET 428
DB  383 HYNMFHYTLDN-ISQKSSVFGNHNV-----TDKLSGLATNIYIFILNVLSDNKYL 434
QY  429 PEY-RVSKADF-----RRVGGPDLYNADGN--GLSRMTIESTPPLVLSHNGV 473
DB  435 NDYNNISKMDFFITNGTRLEKELTAGSQITYDVNKNIFGL-----PILKRRENQ 485
QY  474 RGP-----SHRLS---NAACVYGNRVNVTGTHSLKRENIETANQITQIPAVK 521
DB  486 GNPTLFPYDNYSHILSFKLSIPATYKTQVTFATWTHSSVDPKNTIYTHLTQIPAVK 545
QY  522 SYLLQNYLANAYTVYIKGTHGTGDLIRFLRTKSEYNAVYAGGIRLIINNKTAGOSYRIR 581
DB  546 A-----NSLGTASKVQGPCHTGGDLIDF---KDHF-----KITQHSNFOQSYFIR 589
QY  582 FRYADKAAPFSVYL---YPGGWSGNRFVSLKESYSG-NYDDLKYSDPKFABIITPPLPS 637
DB  590 IRYASNGSANTRAVINLSIPG---VAELGMLNPTFSGTDYTNLKYDKQFYLEFSNEVKFA 647
QY  638 SNIQMDVEMQANSFOSDVNVVLDKIEFLPSNTTILEYEGEDRLEKTKAVNDLFTN 693
DB  648 PNQNISLVNRSVDVYNTNTVLIDKIEFLPITRSIREDEKQKLETVOQIINTFYAN 703
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## RESULT 14

I39811

parasporal crystal protein cry3Bb1 - Bacillus thuringiensis  
N:Alternate names: parasporal crystal protein cryIIIB2  
C:Species: Bacillus thuringiensis



C;Accession: A27323; A26853; A29987; A28407; S60781; I39813  
R;Herrnstadt, C.; Gilroy, T.E.; Sobieski, D.A.; Bennett, B.D.; Gaertner, F.H.  
Gene 57, 37-46, 1987  
A;Title: Nucleotide sequence and deduced amino acid sequence of a coleopteran-active del-  
A;Reference number: A27323; MUID:88112860; PMID:2828180  
A;Accession: A27323  
A;Molecule type: DNA  
A;Residues: 1-652 <HER>  
A;Cross-references: UNIPROT:Q9S6N9; UNIPARC:UPI000000AEDC; GB:M22472; NID:g142733; PID:  
A;Experimental source: strain San Diego  
R;Hoefte, H.; Seuring, J.; Van Houtven, A.; Vaeck, M.  
Nucleic Acids Res. 15, 7183, 1987  
A;Title: Nucleotide sequence of a gene encoding an insecticidal protein of *Bacillus thur*  
A;Reference number: A26953; MUID:98015559; PMID:3658680  
A;Accession: A26953  
A;Molecule type: DNA  
A;Residues: 9-652 <HOE>  
A;Cross-references: UNIPARC:UPI000002B8CD; GB:Y00420; NID:g40252; PIDN:CAA68482.1; PID:G  
A;Experimental source: var. tenebrionis  
R;McPherson, S.A.; Periak, F.J.; Fuchs, R.L.; Marrone, P.G.; Lavrik, P.B.; Fischhoff, D.  
Bio/Technology 6, 61-66, 1988  
A;Title: Characterization of the coleopteran-specific protein gene of *Bacillus thuringie*  
A;Reference number: A29987  
A;Accession: A29987  
A;Molecule type: DNA  
A;Residues: 9-652 <MCP>  
A;Cross-references: UNIPARC:UPI000002B8CD  
A;Experimental source: var. tenebrionis  
R;Sekar, V.; Thompson, D.V.; Maroney, M.J.; Bookland, R.G.; Adang, M.J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 7036-7040, 1987  
A;Title: Molecular cloning and characterization of the insecticidal crystal protein gene  
A;Reference number: A28407  
A;Accession: A28407  
A;Molecule type: DNA  
A;Residues: 9-652 <SEK>  
A;Cross-references: UNIPARC:UPI000002B8CD  
A;Experimental source: var. tenebrionis  
R;Adams, L.F.; Mathewes, S.; O'Hara, P.; Petersen, A.; Guertler, H.  
Mol. Microbiol. 14, 381-389, 1994  
A;Title: Elucidation of the mechanism of CryIIIA overproduction in a mutagenized strain  
A;Reference number: S60781; MUID:95131759; PMID:7930581  
A;Accession: S60781  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 9-652 <ADA>  
A;Cross-references: UNIPARC:UPI000002B8CD; EMBL:U10985; NID:g506182; PIDN:AA43266.1; PI  
A;Experimental source: var. tenebrionis strain NB176, a mutant of strain NB125  
R;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994  
R;Wu, S.J.; Dean, D.H.  
J. Mol. Biol. 255, 628-640, 1996  
A;Title: Functional significance of loops in the receptor binding domain of *Bacillus thur*  
A;Reference number: S62317; MUID:96163559; PMID:8568902  
A;Contents: annotation  
R;Donovan, W.P.; Gonzalez, J.M.  
Mol. Gen. Genet. 214, 365-372, 1988  
A;Title: Isolation and characterization of EG2158, a new strain of *Bacillus thuringiens*  
A;Reference number: I39812; MUID:89112139; PMID:3146015  
A;Accession: I39812  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 9-652 <RES>  
A;Cross-references: UNIPARC:UPI000002B8CD; GB:M37207; NID:g142735; PIDN:AAA50255.1; PID:  
A;Experimental source: strain EG2158  
R;Teixeira De Souza, M.; Lecadet, M.M.; Lereclus, D.  
J. Bacteriol. 175, 2952-2960, 1993  
A;Title: Full expression of the cryIIIA toxin gene of *Bacillus thuringiensis* requires a  
A;Reference number: I39813; MUID:93259939; PMID:8491716  
A;Accession: I39813  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 9-58 <RE2>  
A;Cross-references: UNIPARC:UPI00000B007B; GB:L03393; NID:g304150; PIDN:AAA22350.1; PID:  
C;Genetics:

[illegible]

C;Genetics:  
A;Gene: cryV  
A;Molecule type: DNA  
C;Superfamily: Paraaporal crystal protein  
C;Keywords: Delta-endotoxin

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Best Local Similarity 31.0%; Pred. No. 8.6e-38;  
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Qy 3 KMSGYQNKYEIILESSNNNTNTPNRYPPANNRDMSTMWDCOGISWDIWE---SVET 59  
Db 20 KISTDSLKNETDI-----ELQINIHEDCLKMSEYENVEPVFAST 59

Qy 60 I-TSIGT--NLIEFVIEPSIGGINLLS-IIGKLIPTNRQTVSALSICDLLSIIRKEVAD 115  
Db 60 IQTGIGIAGKILGTGLGVFAQVASLYSIFLGLWPKGKNQWE-IFMEHVEEIIINKIST 118

Qy 116 SVLSDAIADFDGKLNRYEYLSVLGAWLKDGPLOKTNNSDIGQLV--YFVKLSERDEN 173  
Db 119 YARKALTDLKG-LGDALAVYHDSLESWGN-----RNNTRARSVVKSQYIAL-ELMFV 170

Qy 174 EIIGGSLRNNAQVLLPTFAQAANVQLLLRDVAVQYKAQWFPFLSAENVRSBELISPSNG 233  
Db 171 QKL-PSFAVSGEEVPLLPPIYAQAANLHLLLRDASIFGKEW--GLSSSEIST----- 219

Qy 234 CDTGDIYERLCKTBYTYCLYVQVGLNQIKQGGTGADTWSKFNKFRREMTLAVLDI 293  
Db 220 -----FYNQVERAGDYSYHCKWYSTGLNNLR--GTNAESWRYNQFRDRMTLAVLDL 271

Qy 294 IAIPTTYDFEYPLPTHVELTREIYTDVAVG-----YSSGTYSWLRNWPNTFNGLEANG 346  
Db 272 VALFPSDTQYPIKTAQTREYVTDAGTVHPHPSFTSTT--WYNNNAPSFAIEAAV 329

Qy 347 TRGPGVLVLSKIGIYNEYVSR-----YFAGWVGTRHYEDYTKGNGIFQMSGTTSDNLR 401  
Db 330 VRNPHLLDFLEQYIYS-LLSRMSNTQYNNMW-GGHKLEFRITIGGINLSTQGSTWTSIN 387

Qy 402 --NIDFQNAVYKITSIAIMNLVGETTARPEYRVSKADF--RRVGGP---DLNYDAGNNG 454  
Db 388 PVTLPFTSRDVRVYTESLAGLNLF---LTQPVNGVPRVDHFHWKVTPIASDNFYPGYAG 444

Qy 455 LSRMTIESTPPLVHLSNG---VRGSPHRLSNAACVVGNSRVNNYVWTHVTSLKRENIIEA 511  
Db 445 IGTQLQDSENELPEATGQBNYSEYSHRLSHIGLSASHVKALVSWTHRSADRTNTIEP 504

Qy 512 NOITQIPAVKSYLYQNYLANAYTVIKGT-HTCGDLIRFLRTKSEYNAVYVAGGIRLIIN 570  
Db 505 NSITQIPLVKAFNLSSGAA-----VVRGPGFTGDIILRNTTGT-----FGDIRVNIIN 552

Qy 571 NKTAGQSYRIRFYAADKAAFPVYLYPGWGSNRRFVLSKYSYGNV-----DDLKYS 623  
Db 553 PPPA-QRYRVIRIYASTTDLQFHTSI--NGKALNQ-----GNFSATMNRGEDLDYK 600

Qy 624 DFKFAEIIIPPLPSSNIQMDVENQANSFQSDVNVVLDKIEFLPSNTTILEYGERDLEKT 683  
Db 601 TFRVVG-FTPPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVET---YEAEDYFEKA 656

Qy 684 KNAVNDLFTN 693  
Db 657 QEKVTAFTS 666

RESULT 8  
S10228  
paraaporal crystal protein cry3Ba1 - Bacillus thuringiensis (fragment)  
N;Alternate names: coleopteran-active paraaporal crystal protein; delta-endotoxin  
C;Species: Bacillus thuringiensis  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 05-Oct-2004  
C;Accession: S10228  
R;Sick, A.; Gaertner, F.; Wong, A.  
Nucleic Acids Res. 18, 1305, 1990  
A;Title: Nucleotide sequence of a coleopteran-active toxin gene from a new isolate of Ba  
A;Reference number: S10228; MUID:90206811; PMID:2320431

A;Accession: S10228  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-659 <SIC>  
A;Cross-references: UNIPROT:PI7969; UNIPARC:UPI0000126C13; EMBL:X17123; NID:g40258; PID  
C;Genetics:  
A;Gene: cryIIIB  
C;Superfamily: Paraaporal crystal protein  
C;Keywords: delta-endotoxin; toxin

Query Match 17.4%; Score 636; DB 2; Length 659;  
Best Local Similarity 28.6%; Pred. No. 3.9e-35;  
Matches 207; Conservative 141; Mismatches 243; Indels 134; Gaps 34;

Qy 2 KMSPYQNKNEYEILESSNN---TNTPNRYPPANNRD---MSTMWDCOGISWDEIWE 56  
Db 7 RKWNP-NRSEYDTIKVTPNSELPTN-HNQYPLADNPNSTLEELNYKEFLRMTADNSTEV 64

Qy 57 VETIT-----STGINLIEFVI-----EPSLGGINTLI-SIIGKLIPTNRQTVSALSICDLL 106  
Db 65 LDSSTVKDAVGTGISVVGQILGVGVFPFAGALTSFYQSFLNAIWPSDADPWKAF-MAQVE 123

Qy 107 SIIRKEVADSVLSDAIADFDGKLNRYEYLSVLGAWLKDGPLOKTNNSDIGQLVYFVK 166  
Db 124 VLIDKKIEYAKSKALAELOG-LQNNFEDYVNALDSWKKAPVNLRRSQD--KIRELFS 180

Qy 167 LSRDFNEILGGSLSRNNAQVLLPTFAQAANVQLLLRDVAVQYKAQWFPFLSAENVRS 226  
Db 181 QAESHFRNSM-PSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGSEW--GYSSEDI--- 234

Qy 227 LISPNSGCDFTGDIYERLCKTBYTYCLYVQVGLNQIKQGGTGADTWSKFNKFRREM 286  
Db 235 -----AEFYQRLKLTQQYTDHCVNWNVGLNSLR--GSTYDAWVKNFRPRREM 281

Qy 287 TLAVLDLIAIFPTYDPEKYPLPTHVELTREIYTDVAVGSSGTYSWLRNWPNTFNGLEANG 346  
Db 282 TLTVLDLIVLFPFDYVRLYSKGVKTELTRDIFTDPI-----FTLNALQEYGTFTSSIE-NS 336

Qy 347 TRGPGVLVLSKIGIYNEYVSRVYFAGWVGTRHYEDYTKGNGIFQMSGTTSDN----- 399  
Db 337 IRKPHLPDYLRTG-----EFHTRLRPGYSGKDSF-NYWSGNYVETRF-S-IGSNDTITSFFY 390

Qy 400 -----LRNIDFQNAVYKITSIAIMNLVGETTARPEYRVSKADPRRVGGPDLNDYAGN 452  
Db 391 GDKSIEPIQKLSFGDGOKVYR--TIANTDIAAPDGKIYFGVTKVDFSQ-----YDDQK 441

Qy 453 NGLSRMTIESTPPLVHLSNGVRGP-----SHRLSNAACVYVGNR 492  
Db 442 NETSTQTYDSK-----RYNGYLGQAQDSIDQLPPETTDPELXKAYSHQLNTAECLMQDNR 496

Qy 493 --VNVYGWTHTSILKRENIIEANQITQIPAVKSYLYQNYLANAYTVIKGT-HTGGDLIRF 549  
Db 497 GTIPFTWTHRSVDFTNTIDAEEKITQLPVVKAVALSSGAS-----IIEGPGFTGGNLL-F 550

Qy 550 LRTKSEYNNAVYAGGIRLIINNKTKAGQSYRIRFRYAADKAAFPVYLYPGWGSNRRFVSL 609  
Db 551 LKSESSNIAKF-----KVTLSAALLQRYRVIRIYASTT---NLRLFQV-NSNNDPLVI 600

Qy 610 EKSYSQNYD-DLKYSDFKFAEIIIPPLPSSNIQMD-----DVEMQANSFQSDVNVVLDK 661  
Db 601 YINKTNWIDGDLTYOTDFDA-----TSNSNMGFGSDTNDFTIIGAESFVSNKEIYIDK 652

Qy 662 IEFLP 666  
Db 653 IEFIP 657

RESULT 9  
A27323  
paraaporal crystal protein cry3Ba1 - Bacillus thuringiensis  
N;Alternate names: coleopteran-specific insect control protein; crystal protein cryC; d  
C;Species: Bacillus thuringiensis  
C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 05-Oct-2004



QY	70	FVI-----EPISGGINTLLS-IIGKLIPTNRQTVSALSICDLLSIIRKEVADSVLSDAIAD	124
Db	60	RIIGLVGPVAGQVASYSLVGLWPRGRDQWE-IPLEHVEQLNQIITENARNTALAR	118
QY	125	FDGKLKNRYEYLYSLGAWLKDGKPLQKTNNSDIGQLVY--YFKLSERDFNEILGGSLSR	182
Db	119	LOGLGDSFRAYQQS-LEDW-----LENRDDARTSRVLYTQYIAL-ELDFLNAMPLFAIR	170
QY	183	NNAQVLLPTFAQANVQLLLRDAVOYKAQWFFFLSAENVRSELISPNCGDFTGDYYE	242
Db	171	NQ-EVPLLMVYAQAANLHLLLRDASLFGSE-FGLTSQEIQR-----YYE	213
QY	243	RLKCKTAETNYCLYVYQVGLNQIKOGGTGADTWSKENKERREMTLAVLDIIAIFPTDYF	302
Db	214	QOVERTKDYSDYCVEMTNTGLNSR--GTNAASWVRYNQPRDLTLGLVLDLVALFPSTYT	271
QY	303	EKYPPLTHVELTREIYTDVAV---GYSGCTYSWLRNMPNTENGLEANGTRGPGVLVWLSKI	359
Db	272	RTYPINTSAQLTREVTYDAIGATGVNMAWMNWNNAAPSASEAAIRSPHLLDFLEQL	331
QY	360	GIINEYVSRVPAGWGRHRYEDYTKNGIFORMSG-----TTSNDLRNIDFQNA	408
Db	332	TIFSA-----SSRWSNTRHM-TYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLRFASR	385
QY	409	DVYKITSLAIMNLVGETTARPEYRVSKADFRVRVGGPDLDNYDAG-----NGLSRMT	459
Db	386	DVTRTESYAGVLWG-IYLEPIHGVTFRFNTNPQNIS--DRGTANYSQPYESPGQLKD	443
QY	460	IESTF-PLVLHNGVRGSPHRLNAAACVYVGNRSRVNVYGWHTPSLKRNIIEANQITQIP	518
Db	444	SETELPPEITERPNYSYSHRLSHIGIILQSRVNVVPYSWTHRSADRTWTIGNRIQIP	503
QY	519	AVKSYVLQNYLANAYTVYIKGT-HTGGDLIRFLRTKSEYNAVYAGGIRLIINNKTAGOS	577
Db	504	MVKASELPQ-----GTTVRGPGFTGGDILR--RTWTG-----GFGPIRVTVNGPLT-QR	550
QY	578	YRIRPYAADKAAPFSVLYPGWGSNRPVLSLEKSYSGNYDLDKYDFKAEIITPPLPS	637
Db	551	YRIGFRYAS--TVDFOFFVSRGGTTVNNRFLRTMNSG--DELKYNF-VRRAFITPPTF	605
QY	638	SNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTTLVEYGERDLEKTKNAVNDLFTN	693
Db	606	TQIQDIIRTSIQLSNGEVIYDKIEIIP---VTATFEAYDLERAQEAVALFTN	658
RESULT 4			
I39815			
insecticidal protein cryV - Bacillus thuringiensis			
C:Species: Bacillus thuringiensis			
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 05-Oct-2004			
C:Accession: I39815			
R:Gleave, A.P.; Williams, R.; Hedges, R.J.			
Appl. Environ. Microbiol. 59, 1683-1687, 1993			
A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for			
iensis subsp. kurstaki.			
A:Reference number: I39815; MUID:93298009; PMID:8517758			
A:Accession: I39815			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: DNA			
A:Residues: 1-719 <RES>			
A:Cross-references: UNIPROT:Q45752; UNIPARC:UPI0000036008; GB:M98544; NID:g142767; PIDN:			
C:Gene: cryV			
C:Superfamily: Parasporal crystal protein			
Query Match 18.6%; Score 679; DB 2; Length 719;			
Best Local Similarity 31.0%; Pred. No. 5.4e-38;			
Matches 226; Conservative 119; Mismatches 263; Indels 122; Gaps 33;			
QY	3	KMSYPQNKNEYETLESSNNNTNTPNRYPPFANNRDMSTMSWNCQGISWDEIWE---SVET	59
Db	20	KISTDSLKNETDI-----ELQNIHNEDECLKSEYENVPEPFVSAST	59

QY	60	I-TSIGI--NLIEFVIEPSLGGINTLLS-IIGKLIPTNRQTVSALSICDLLSIIRKEVAD	115
Db	60	IQTGIGIAGIKILGTLGVPAGQVASYSLFGLBWPKGKNQWE-IFMEHVEEIIINOKIST	118
QY	116	SVLSDAIADPDGKLNRYEYLYSLGAWLKDGKPLQKTNNSDIGQLV--YFKLSERDFN	173
Db	119	YARNKALTDLKG-LGDALAVYHDSLESVGN-----RNNTRARSVVKSYIAL-ELMFV	170
QY	174	EILGGSLSRNAQVLLPTFAQANVQLLLRDAVOYKAQWFFFLSAENVRSELISPSNG	233
Db	171	OKL-PSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEM--GLSSEIST-----	219
QY	234	CDFTGDYERLCKTAETNYCLYVYQVGLNQIKOGGTGADTWSKFNKFRREMTLAVLDI	293
Db	220	-----FYNRQVERAGDYSCHCKVYSTGLNNLR--GTNAESWVRYNQFRDRDTLMLVDL	271
QY	294	IAIFPTYDPEKYPPLTHVELTREIYTDVAV-----YSSGTYSWLRNMPNTENGLEANG	346
Db	272	VALFPSTYDQMPYIKTTAQLTREVTYDAIGTVHPHPSFTSTT--WYNNNAPSFAIEAAV	329
QY	347	TRGPGVLVWLSKIGIYNEYSR-----YPAGWVGRHRYEDYTKNGIFORMSGTTSNDLR	401
Db	330	VRNPHLLDLEQVTIYS-LLSRWSNTQYNNMM-GGHKLEFRTIGGLTINISTQGSTWTSIN	387
QY	402	--NIDFQNDVTKITSLAIMNLVGETTARPEYRVSKADF--RRVGGP----DLNYDAGNNG	454
Db	388	PVTLPTSTRDVTYRTESLAGNLF--LTQPVNGVPRVDFHWKFPVTHPIASDNPYPYGYAG	444
QY	455	LSRMTIESFPVLVLSNG---VRGPSHRLSNAACVYVGNRSRVNVYGWHTPSLKRNIIEA	511
Db	445	ICTQDSSENEUPPATGQPNYESYSHRLSHGLISASHVKALVSWTHRSADRTWTIEP	504
QY	512	NQITQIPAVKSYVLQNYLANAYTVYIKGT-HTGGDLIRFLRTKSEYNAVYAGGIRLIIN	570
Db	505	NSITQIPLVKAFNLSSGAA-----VVRGPGFTGGDILRRTNIGT-----FGDIRVIN	552
QY	571	NKTACQSVTRIRPYAADKAAPFSVLYPGWGSNRPVLSLEKSYSGNY-----DDLKYS	623
Db	553	PPFA-QRYVRVIRYASTTDLPHTSI--NGKAINQ-----GNFSATMNRGEDLDYK	600
QY	624	DFKFAEITPPLPSSNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTTLVEYGERDLEKT	683
Db	601	TPRTVG-FTTPSPFLDVQSTFTTIGAWNFSSGNEVIDRIEFVPEVET---YEAEDFEKA	656
QY	684	KNAVNDLFTN	693
Db	657	QEKVTALFTS	666
RESULT 5			
I40590			
cryV465 protein - Bacillus thuringiensis			
C:Species: Bacillus thuringiensis			
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Oct-2004			
C:Accession: I40590			
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.			
Appl. Environ. Microbiol. 61, 2402-2407, 1995			
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis			
tomocidus.			
A:Reference number: I39814; MUID:95314293; PMID:7793960			
A:Accession: I40590			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: DNA			
A:Residues: 1-719 <RES>			
A:Cross-references: UNIPROT:Q45709; UNIPARC:UPI000003600C; EMBL:U07642; NID:g467234; PI:			
C:Gene: cryV465			
C:Superfamily: Parasporal crystal protein			
Query Match 18.6%; Score 678.5; DB 2; Length 719;			
Best Local Similarity 30.8%; Pred. No. 5.8e-38;			
Matches 226; Conservative 119; Mismatches 281; Indels 107; Gaps 31;			

QY 177 ---GSLSRNAQVLLPTFAQANVQLLLRDVAVQKAW-----FPFLSAENVRSLEI 228  
 DB 175 LINGSLARQNAQVLLPTFAQANVQLLLRDVAVQKAW-----FPFLSAENVRSLEI 234  
 QY 229 SPNSGCDFTGDYERLCKTAETNYCLYVYQVGLNQIKQGGTADTWKFNKFRREMTL 288  
 DB 235 E-----LYTDYCVHYNRGFNELRQGTGSATAWLEPHRYRREMTL 274  
 QY 289 AVLDIIAIPPTYDEKYPPLTHVELTREIYTDVGY-----SGTYSWLR--NWPNTFNL 342  
 DB 275 MVLDIVASPSLIDITNPIETDQSLSRVITDPIGFVHRSSLRGESWFSFVNAN--FSDL 333  
 QY 343 EANGTRGGLVTLWSKIGIYNEVSRYPAG-----WVGRHYEDYTKNGIFQBMST 395  
 DB 334 E-NAIENPRPSWFLNNWISTGSLTLPVSPSTRARVWYGSRRDISPANSQFTELISQ 392  
 QY 396 TSNLDNRIDFQADVYKITSALIMNLVGETTARPEYRVSADFRVGGPDLNVDAGNGL 455  
 DB 393 HTTATQTLGRN--IFRVDQA--CNL-NDTT---YGNRAVP-----YHDASEGS 435  
 QY 456 SMTIESTPLVLSHNGVRP-----SHRLSNAACVYVG-----489  
 DB 436 QRSVYEG---YRTTGIDNPRVQNTYLPGENSDIPTPEDVTHILSTTLNLTGLRQV 491  
 QY 490 ---NSRVNVYGTWHTSLKRENIIEANOITQIPAVKSYLQVLANAYTVYIKGTHGCD 545  
 DB 492 ASNRSSLYMGWTHKSLARNNTINPDRIQTPLTK-----VDTGTGVSVDNPOFIGGA 547  
 QY 546 LIRFLRTKSEYNAVAGGGIRLIIINNTAGQSYRIRFRYAADKAAPFVSYLPGGWSNR 605  
 DB 548 LLQ-----RVDHGLS-----GVLRVQFPLHLRQYRIRVRYASTNRLSV-----NGS 591  
 QY 606 FVLSLEKSYSGNY---DDLKYSDFKFAELITPPLP--SSNQMDVEMQANSFQSDVNVLDK 661  
 DB 592 FGTISQNLPSLWRLGDLRYGSFAIREFNTSIRTPASPDQIRLTIEPSIRQEVV--DR 649  
 QY 662 IEFLPSNTTLEVEGERDELEKTKNAVNDLFT 692  
 DB 650 IEFIPVNPTR---EAKEDLEAKKAVASLFT 677  
 RESULT 2  
 I40589  
 parasporal crystal protein cry8Cal - Bacillus thuringiensis  
 N:Alternate names: parasporal crystal protein cryIII  
 C:Species: Bacillus thuringiensis  
 C>Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Oct-2004  
 C:Accession: I40589  
 R:Sato, R.; Takeuchi, K.; Ogiwara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Hori, H.; Asano  
 Curr. Microbiol. 28, 15-19, 1994  
 A:Title: Cloning, heterologous expression, and localization of a novel crystal protein g  
 A:Reference number: I40589; MUID:94100786; PMID:7764305  
 A:Accession: I40589  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1160 <RES>  
 A:Cross-references: UNIPROT:Q45706; UNIPARC:UPI0000126CPE; EMBL:U04366; NID:G532523; PID  
 C:Superfamily: Parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match 19.9%; Score 728.5; DB 2; Length 1160;  
 Best Local Similarity 29.9%; Pred. No. 4.7e-41;  
 Matches 232; Conservative 124; Mismatches 240; Indels 179; Gaps 34;  
 QY 4 MSPYQNKNEYEILESSNNNTNPN--RYPFANNRDMSTMSWDCQGISWDE-----52  
 DB 1 MSP-NNQNEYEILDALSPVSNSIRYPLANDQNTLQNMKYKYLKMTSTNAELSRN 59  
 QY 53 --IWSEVETITIGINLIEFVIE---PSLGGINTLL-SIIKGLIPTNRQTVSALSICDL 105  
 DB 60 PGTFISAQAVGTGDIVSTIISGLGIPVLGEVFSILGSLIGLLWPSNNENWQIFMNRV 119

QY 106 LSIIRKEVADSVLDAIDFDGKLKNYR---EYLSYLGAWLKDGKPLQKTNNSDIGQLV 162  
 DB 120 ELIDQKILDSVRSRAIAD---LANSRIAVEYYQNALEDWRKNP---HSTRSAAL----168  
 QY 163 YFKLSERDFN--ETLG---GSLSRNAQVLLPTFAQANVQLLLRDVAVQKAWPFP 217  
 DB 169 ---VKERFGNAELRLTNMGFSQTNVETPLPTPYAQAASLHLLVMDRVQIYGKEWG--222  
 QY 218 LSAENVRSLEISPNSGCDFTGDYERLCKTAETNYCLYVYQVGLNQIKQGGTADTW 277  
 DB 223 ---YQNDIDL---FYKEQVSRYTARYSDHCQVQWYNAGLNKLK--GTGAKQWV 266  
 QY 278 KENFEREMTLAVLDIIAIPPTYDEKYPPLTHVELTREIYTDVGY-----YSSGTYSWLRNWP 336  
 DB 267 DYNRFRREMNVMVLDLVALFPNDYARIYPLETNAELTREIETDPVGSVYVTCQSSTLISWY 326  
 QY 337 N-----TFNGLEANGTRGPGVTLWSKIGIYNEY---VSRYPAGWVGTRHYEDYTKG 385  
 DB 327 DMIPALPSPSTLE-NLRLKDPDFLLQEIEMKYSFRONGTIEYNYNGGQRLTISYIG 385  
 QY 386 NGIFORMSGTSTNLDNRIDFQADVYKI-----TSALIMNLVGETTAR 428  
 DB 386 SS-FNKYSGLVAGABDIIPVQNDIYRVVTVIGRYTNSLLGVNPDVTFVFSNNTQKYSK 444  
 QY 429 PEY---RVSKADFRVGGPDL---NYDAGNGLSRMT---TESTPPLVLSHNGVRGPHR 479  
 DB 445 PKQFAGGIKTID---SGBELTYENYQSYSHRVSYITSFEIKSTGGTVL---GV-----491  
 QY 480 LSNACVYVYGNRVNVYGTWHTSLKRENIIEANOITQIPAVKSYLQVLANAYTVYIKG 539  
 DB 492 ---VPIFGWTHSSARRNFVATKISQIPINKA---SRTSGGAVNWFQEG 535  
 QY 540 THTGDLRLFRUTKSEYNNAVYAGG-----IRLIINNTAGQSYRIRFRYAADKAAPFVS 594  
 DB 536 LYNGGPNVVKL-----SGSGSVINLRVATDAKASQRYRIRIRYASDRAGKFTI 584  
 QY 595 YLPGWGSNRFVLSLEKSYSGNY-----DDLKYSDFKFAELITPPLSSNQMDVE 645  
 DB 585 ---SSRSPENPATYSIAIYNTMTSNASLTYSTPAYAE-----SGPINLGIS 629  
 QY 646 MQANSFQSDV-----NVLDKIEFLPSNTTLEVEGERDELEKTKNAVNDLFTN 693  
 DB 630 GSSRTFDISITKEAGANLYIDRIEPIPVNTL---FEAEEDLDVAKAVNGLFTN 681  
 RESULT 3  
 S00873  
 parasporal crystal protein cry8a - Bacillus thuringiensis subsp. thuringiensis  
 N:Alternate names: parasporal crystal protein cryA4  
 C:Species: Bacillus thuringiensis subsp. thuringiensis  
 C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 05-Oct-2004  
 C:Accession: S00873  
 R:Brizzard, B.L.; Whiteley, H.R.  
 Nucleic Acids Res. 16, 2723-2724, 1988  
 A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus  
 A:Reference number: S00873; MUID:88203216; PMID:3362680  
 A:Accession: S00873  
 A:Molecule type: DNA  
 A:Residues: 1-1228 <BRI>  
 A:Cross-references: UNIPROT:P05517; UNIPARC:UPI0000126BDC; EMBL:X06711; NID:G40264; PIDN  
 C:Genetics:  
 A:Gene: cryA4  
 A:Start codon: TTG  
 C:Superfamily: Parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match 19.3%; Score 705.5; DB 2; Length 1228;  
 Best Local Similarity 31.3%; Pred. No. 1.9e-39;  
 Matches 224; Conservative 118; Mismatches 279; Indels 95; Gaps 31;  
 QY 10 KNEYEILESSNNNTNPNRYPFANNRDMSTMSWDCQGISWDEIWSVETITIGINLIE 69  
 DB 6 KNEEINAVNSHSAQMDLLPDARIEDSLCTA---EGNNIDP-FVSASTVQT-GINTAG 59

